

**Figure 1A****4.1.1 Heavy Chain DNA**

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ATGGAGTTTG GGCTGAGCTG GGTTCCTC GTTGCTCTTT TAAGAGGTGT 50
CCAGTGTGAG GTGCAGCTGG TGGAGTCTGG GGGAGGCGTG GTCCAGCCTG 100
GGAGGTCCCT GAGACTCTCC TGTGTAGCGT CTGGATTAC CTTCAGTAGC 150
CATGGCATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC TGGAGTGGGT 200
GGCAGTTATA TGGTATGATG GAAGAAATAA ATACTATGCA GACTCCGTGA 250
AGGGCCGATT CACCATCTCC AGAGACAATT CCAAGAACAC GCTGTTTCTG 300
CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTGTATT ACTGTGCGAG 350
AGGAGGTCAC TTCGGTCCTT TTGACTACTG GGGCCAGGGA ACCCTGGTCA 400
CCGTCTCCTC AGCCTCCACC AAGGGCCCAT CGGTCTTCCC CCTGGCGCCC 450
TGCTCCAGGA GCACCTCCGA GAGCACAGCG GCCCTGGGCT GCCTGGTCAA 500
GGACTACTTC CCCGAACCGG TGACGGGTGTC GTGGAAGTCA GGCCTCTGA 550
CCAGCGGCGT GCACACCTTC CCAGCTGTCC TACAGTCCTC AGGACTCTAC 600
TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAACTTCG GCACCCAGAC 650
CTACACCTGC AACGTAGATC ACAAGCCAG CAACACCAAG GTGGACAAGA 700
CAGTTGAGCG CAAATGTTGT GTCGAGTGCC CACCGTGCCC AGCACCACCT 750
GTGGCAGGAC CGTCAGTCTT CCTCTTCCCC CAAAACCCA AGGACACCCT 800
CATGATCTCC CGGACCCCTG AGGTCACGTG CGTGGTGGTG GACGTGAGCC 850
ACGAAGACCC CGAGGTCCAG TTCAACTGGT ACGTGGACGG CGTGGAGGTG 900
CATAATGCCA AGACAAAGCC ACGGGAGGAG CAGTTCAACA GCACGTTCCG 950
TGTGGTCAGC GTCCTCACCG TTGTGCACCA GGAAGTGGTG AACGGCAAGG 1000
AGTACAAGTG CAAGGTCTCC AACAAAGGCC TCCCAGCCCC CATCGAGAAA 1050
ACCATCTCCA AAACCAAAGG GCAGCCCCGA GAACCACAGG TGTACACCCT 1100
GCCCCATCC CGGGAGGAGA TGACCAAGAA CCAGGTCAGC CTGACCTGCC 1150
TGGTCAAAGG CTTCTACCCC AGCGACATCG CCGTGGAGTG GGAGAGCAAT 1200
GGGCAGCCGG AGAACAATA CAAGACCACA CCTCCCATGC TGGACTCCGA 1250
CGGCTCCTTC TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC 1300
AGCAGGGGAA CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC 1350
CACTACACGC AGAAGAGCCT CTCCCTGTCT CCGGGTAAAT GA 1392

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(SEQ ID NO:27)

**4.1.1 Heavy Chain Protein**

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MEFGLSWVFL VALLRGVQCQ VQLVESGGGV VQPGRSLRLS CVASGFTFSS 50
HGMHWVRQAP GKGLEWVAVI WYDGRNKYYA DSVKGRFTIS RDNSKNTLFL 100
QMNSLRAEDT AVYYCARGGH FGPFDYWQGG TLVTVSSAST KGPSVFPLAP 150
CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 200
SLSSVVTVPV SNFGTQTYTC NVDHKPSNTK VDKTVERKCC VECPPCPAPP 250
VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ FNWYVDGVEV 300
HNAKTKPREE QFNSTFRVVS VLTGVHQLDWL NGKEYKCKVS NKGLPAPIEK 350
TISKTKGQPR EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN 400
GQPENNYKTT PPMILDSGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN 450
HYTQKSLSL PGK 463

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(SEQ ID NO:1)

**Figure 1A** (continued)**4.1.1 Kappa Chain DNA**

```

ATGGAAACCC CAGCGCAGCT TCTCTTCCTC CTGCTACTCT GGCTCCCAGA 50
TACCACCGGA GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT 100
CTCCAGGGGA AAGAGCCACC CTCTCCTGCA GGGCCAGTCA GAGTATTAGC 150
AGCAGCTTCT TAGCCTGGTA CCAGCAGAGA CCTGGCCAGG CTCCCAGGCT 200
CCTCATCTAT GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA 250
GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG 300
CCTGAAGATT TTGCAGTGTA TTA CTGTCAG CAGTATGGTA CCTCACCTG 350
GACGTTCCGC CAAGGGACCA AGGTGGAAAT CAAACGAACT GTGGCTGCAC 400
CATCTGTCTT CATCTTCCCG CCATCTGATG AGCAGTTGAA ATCTGGA ACT 450
GCCTCTGTTG TGTGCCTGCT GAATAACTTC TATCCCAGAG AGGCCAAAGT 500
ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC CAGGAGAGTG 550
TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTG 600
ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT 650
CACCCATCAG GGCCTGAGCT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG 700
AGTGTTAG 708

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(SEQ ID NO:40)

**4.1.1 Kappa Chain Protein**

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METPAQLLFL LLLWLPD TTG EIVLTQSPGT LSLSPGERAT LSCRASQ SIS 50
SSFLAWYQQR PGQAPRL LIY GASSRATGIP DRFSGSGSGT DFTLTISRLE 100
PEDFAVYYCQ QYGTSPWTFG QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT 150
ASVVCLLN NF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL 200
TLISKADYEKH K VYACEVTHQ GLSSPVTKSF NRGEC 235

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(SEQ ID NO:14)

**Figure 1B****4.8.1 Heavy Chain DNA**

|                   |                   |                   |                    |                   |      |
|-------------------|-------------------|-------------------|--------------------|-------------------|------|
| <b>ATGGAGTTTG</b> | <b>GGCTGAGCTG</b> | <b>GGTTTTCTC</b>  | <b>GTTGCTCTTT</b>  | <b>TAAGAGGTGT</b> | 50   |
| <b>CCAGTGTGAG</b> | <b>GTGCAGCTGG</b> | <b>TGGAGTCTGG</b> | <b>GGGAGGCGTG</b>  | <b>GTCCAGCCTG</b> | 100  |
| <b>GGAGGTCCCT</b> | <b>GAGACTCTCC</b> | <b>TGTACAGCGT</b> | <b>CTGGATTAC</b>   | <b>CTTCAGTAAC</b> | 150  |
| <b>TATGGCATGC</b> | <b>ACTGGGTCCG</b> | <b>CCAGGCTCCA</b> | <b>GGCAAGGGGC</b>  | <b>TGGAGTGGGT</b> | 200  |
| <b>GGCAGTTATA</b> | <b>TGGTATGATG</b> | <b>GAAGTAATAA</b> | <b>ACACTATGGA</b>  | <b>GACTCCGTGA</b> | 250  |
| <b>AGGGCCGATT</b> | <b>CACCATCTCC</b> | <b>AGTGACAATT</b> | <b>CCAAGAACAC</b>  | <b>GCTGTATCTG</b> | 300  |
| <b>CAAATGAACA</b> | <b>GCCTGAGAGC</b> | <b>CGAGGACACG</b> | <b>GCTGTGTATT</b>  | <b>ACTGTGCGAG</b> | 350  |
| <b>AGGAGAGAGA</b> | <b>CTGGGGTCTC</b> | <b>ACTTTGACTA</b> | <b>CTGGGGGCCAG</b> | <b>GGAACCCTGG</b> | 400  |
| <b>TCACCGTCTC</b> | <b>CTCAGCCTCC</b> | <b>ACCAAGGGCC</b> | <b>CATCGGTCTT</b>  | <b>CCCCCTGGCG</b> | 450  |
| <b>CCCTGCTCCA</b> | <b>GGAGCACCTC</b> | <b>CGAGAGCACA</b> | <b>GCGGCCCTGG</b>  | <b>GCTGCCTGGT</b> | 500  |
| <b>CAAGGACTAC</b> | <b>TTCCCCGAAC</b> | <b>CGGTGACGGT</b> | <b>GTCGTGGAAC</b>  | <b>TCAGGCGCTC</b> | 550  |
| <b>TGACCAGCGG</b> | <b>CGTGACACAC</b> | <b>TTCCCAGCTG</b> | <b>TCCTACAGTC</b>  | <b>CTCAGGACTC</b> | 600  |
| <b>TACTCCCTCA</b> | <b>GCAGCGTGGT</b> | <b>GACCGTGCCC</b> | <b>TCCAGCAACT</b>  | <b>TCGGCACCCA</b> | 650  |
| <b>GACCTACACC</b> | <b>TGCAACGTAG</b> | <b>ATCACAAGCC</b> | <b>CAGCAACACC</b>  | <b>AAGGTGGACA</b> | 700  |
| <b>AGACAGTTGA</b> | <b>GCGCAAATGT</b> | <b>TGTGTCGAGT</b> | <b>GCCCCACGTG</b>  | <b>CCCAGCACCA</b> | 750  |
| <b>CCTGTGGCAG</b> | <b>GACCGTCAGT</b> | <b>CTTCCTCTTC</b> | <b>CCCCCAAAC</b>   | <b>CCAAGGACAC</b> | 800  |
| <b>CCTCATGATC</b> | <b>TCCCGGACCC</b> | <b>CTGAGGTCAC</b> | <b>GTGCGTGGTG</b>  | <b>GTGGACGTGA</b> | 850  |
| <b>GCCACGAAGA</b> | <b>CCCCGAGGTC</b> | <b>CAGTTCAACT</b> | <b>GGTACGTGGA</b>  | <b>CGGCGTGGAG</b> | 900  |
| <b>GTGCATAATG</b> | <b>CCAAGACAAA</b> | <b>GCCACGGGAG</b> | <b>GAGCAGTTCA</b>  | <b>ACAGCACGTT</b> | 950  |
| <b>CCGTGTGGTC</b> | <b>AGCGTCCTCA</b> | <b>CCGTTGTGCA</b> | <b>CCAGGACTGG</b>  | <b>CTGAACGGCA</b> | 1000 |
| <b>AGGAGTACAA</b> | <b>GTGCAAGGTC</b> | <b>TCCAACAAAG</b> | <b>GCCTCCAGC</b>   | <b>CCCCATCGAG</b> | 1050 |
| <b>AAAACCATCT</b> | <b>CCAAAACCAA</b> | <b>AGGGCAGCCC</b> | <b>CGAGAACCAC</b>  | <b>AGGTGTACAC</b> | 1100 |
| <b>CCTGCCCCCA</b> | <b>TCCCGGGAGG</b> | <b>AGATGACCAA</b> | <b>GAACCAGGTC</b>  | <b>AGCCTGACCT</b> | 1150 |
| <b>GCCTGGTCAA</b> | <b>AGGCTTCTAC</b> | <b>CCCAGCGACA</b> | <b>TCGCCGTGGA</b>  | <b>GTGGGAGAGC</b> | 1200 |
| <b>AATGGGCAGC</b> | <b>CGGAGAACAA</b> | <b>CTACAAGACC</b> | <b>ACACCTCCCA</b>  | <b>TGCTGGACTC</b> | 1250 |
| <b>CGACGGCTCC</b> | <b>TTCTTCCTCT</b> | <b>ACAGCAAGCT</b> | <b>CACCGTGGAC</b>  | <b>AAGAGCAGGT</b> | 1300 |
| <b>GGCAGCAGGG</b> | <b>GAACGTCTTC</b> | <b>TCATGCTCCG</b> | <b>TGATGCATGA</b>  | <b>GGCTCTGCAC</b> | 1350 |
| <b>AACCACTACA</b> | <b>CGCAGAAGAG</b> | <b>CCTCTCCCTG</b> | <b>TCTCCGGGTA</b>  | <b>AATGA</b>      | 1395 |

(SEQ ID NO:28)

**4.8.1 Heavy Chain Protein**

|                   |                   |                   |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| <b>MEFGLSWVFL</b> | <b>VALLRGVQCQ</b> | <b>VQLVESGGGV</b> | <b>VQPGRSLRLS</b> | <b>CTASGFTFSN</b> | 50  |
| <b>YGMHWVRQAP</b> | <b>GKGLEWVAVI</b> | <b>WYDGSNKHYG</b> | <b>DSVKGRFTIS</b> | <b>SDNSKNTLYL</b> | 100 |
| <b>QMNSLRAEDT</b> | <b>AVYYCARGER</b> | <b>LGSYFDYWQ</b>  | <b>GTLVTVSSAS</b> | <b>TKGPSVFPLA</b> | 150 |
| <b>PCSRSTSEST</b> | <b>AALGCLVKDY</b> | <b>FPEPVTVSWN</b> | <b>SGALTSGVHT</b> | <b>FPAVLQSSGL</b> | 200 |
| <b>YSLSSVVTVP</b> | <b>SSNFGTQTYT</b> | <b>CNVDHKPSNT</b> | <b>KVDKTVKRC</b>  | <b>CVECPPCPAP</b> | 250 |
| <b>PVAGPSVFLF</b> | <b>PPKPKDTLMI</b> | <b>SRTPEVTCVV</b> | <b>VDVSHEDPEV</b> | <b>QFNWYVDGVE</b> | 300 |
| <b>VHNAKTKPRE</b> | <b>EQFNSTFRVV</b> | <b>SVLTVVHQDW</b> | <b>LNGKEYKCKV</b> | <b>SNKGLPAPIE</b> | 350 |
| <b>KTISKTKGQP</b> | <b>REPQVYTLPP</b> | <b>SREEMTKNQV</b> | <b>SLTCLVKGFY</b> | <b>PSDIAVEWES</b> | 400 |
| <b>NGQPENNYKT</b> | <b>TPPMLDSGDS</b> | <b>FFLYSKLTVD</b> | <b>KSRWQQGNVF</b> | <b>SCSVMHEALH</b> | 450 |
| <b>NHYTQKSLSL</b> | <b>SPGK</b>       |                   |                   |                   | 464 |

(SEQ ID NO:2)

**Figure 1B** (continued)**4.8.1 Kappa Chain DNA**

```

ATGGAACCC CAGCGCAGCT TCTCTTCCTC CTGCTACTCT GGCTCCCAGA 50
TACCACCGGA GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT 100
CTCCAGGGGA AAGAGCCACC CTCTCCTGCA GGACCAGTGT TAGCAGCAGT 150
TACTTAGCCT GGTACCAGCA GAAACCTGGC CAGGCTCCCA GGCTCCTCAT 200
CTATGGTGCA TCCAGCAGGG CCACTGGCAT CCCAGACAGG TTCAGTGGCA 250
GTGGGTCTGG GACAGACTTC ACTCTCACCA TCAGCAGACT GGAGCCTGAA 300
GATTTTGCAG TCTATTACTG TCAGCAGTAT GGCATCTCAC CCTTCACTTT 350
CGGCGGAGGG ACCAAGGTGG AGATCAAGCG AACTGTGGCT GCACCATCTG 400
TCTTCATCTT CCCGCCATCT GATGAGCAGT TGAAATCTGG AACTGCCTCT 450
GTTGTGTGCC TGCTGAATAA CTTCTATCCC AGAGAGGCCA AAGTACAGTG 500
GAAGGTGGAT AACGCCCTCC AATCGGGTAA CTCCCAGGAG AGTGTACACAG 550
AGCAGGACAG CAAGGACAGC ACCTACAGCC TCAGCAGCAC CCTGACGCTG 600
AGCAAAGCAG ACTACGAGAA ACACAAAGTC TACGCCTGCG AAGTCACCCA 650
TCAGGGCCTG AGCTCGCCCG TCACAAAGAG CTTCAACAGG GGAGAGTGTT 700
AG

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(SEQ ID NO:41)

**4.8.1 Kappa Chain Protein**

```

METPAQLLFL LLLWLPDTTG EIVLTQSPGT LSLSPGERAT LSCRTSVSSS 50
YLAWYQQKPG QAPRLLIYGA SSRATGIPDR FSGSGSGTDF TLTISRLEPE 100
DFAVYYCQQY GISPFTFGGG TKVEIKRTVA APSVFIFPPS DEQLKSGTAS 150
VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL 200
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC 233

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(SEQ ID NO:15)

**Figure 1C****4.14.3 Heavy Chain DNA**

```

CCTGGGAGGT CCCTGAGACT CTCCTGTGCA GCGTCTGGAT TCACCTTCAG 50
TAGTCATGGC ATCCACTGGG TCCGCCAGGC TCCAGGCAAG GGGCTGGAGT 100
GGGTGGCAGT TATATGGTAT GATGGAAGAA ATAAAGACTA TGCAGACTCC 150
GTGAAGGGCC GATTCAACCAT CTCCAGAGAC AATTCCAAGA AGACGCTGTA 200
TTTGCAAATG AACAGCCTGA GAGCCGAGGA CACGGCTGTG TATTACTGTG 250
CGAGAGTGGC CCCACTGGGG CCACTTGACT ACTGGGGCCA GGGAACCCTG 300
GTCACCGTCT CCTCAGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 350
GCCCTGCTCC AGGAGCACCT CCGAGAGCAC AGCGGCCCTG GGCTGCCTGG 400
TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCT 450
CTGACCAGCG GCGTGCACAC CTTCCCAGCT GTCCTACAG 489

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(SEQ ID NO:29)

**4.14.3 Heavy Chain Protein**

```

PGRSLRLSCA ASGFTFSSHG IHWVRQAPGK GLEWVAVIWY DGRNKDYADS 50
VKGRFTISRD NSKKTLYLQM NSLRAEDTAV YYCARVAPLG PLDYWGQGT 100
VTVSSASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA 150
LTSGVHTFPA VLQ 163

```

(SEQ ID NO:3)

**4.14.3 Kappa Chain DNA**

```

GGCACCCCTGT CTTTGTCTCC AGGGGAAAGA GCCACCCCTCT CCTGCAGGGC 50
CAGTCAGAGT GTCAGCAGCT ACTTAGCCTG GTACCAGCAG AAACCTGGCC 100
AGGCTCCCAG ACTCCTCATC TATGGTGCAT CCAGCAGGGC CACTGGCATC 150
CCAGACAGGT TCAGTGGCAG TGGGTCTGGG ACAGACTTCA CTCTCACCAT 200
CAGCAGACTG GAGCCTGAGG ATTTTGCAGT GTATTACTGT CAGCAGTATG 250
GTAGGTCACC ATTCACTTTC GGCCCTGGGA CCAAAGTGGA TATCAAGCGA 300
ACTGTGGCTG CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT 350
GAAATCTGGA ACTGCCTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA 400
GAGAGGCCAA AGTACAG 417

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(SEQ ID NO:42)

**4.14.3 Kappa Chain Protein**

```

GTLSSLSPGER ATLSCLASQS VSSYLAWYQQ KPGQAPRLLI YGASSRATGI 50
PDRFSGSGSG TDFTLTISRL EPEDFAVYYC QQYGRSPFTF GPGTKVDIKR 100
TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQ 139

```

(SEQ ID NO:16)

## Figure 1D

### 6.1.1 Heavy Chain DNA

|            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------|
| ATGGAGTTTG | GGCTGAGCTG | GGTTTTCTC  | GTTGCTCTTT | TAAGAGGTGT | 50   |
| CCAGTGTCAG | GTGCAGCTGG | TGGAGTCTGG | GGGAGGCGTG | GTCGAGCCTG | 100  |
| GGAGGTCCCT | GAGACTCTCC | TGTACAGCGT | CTGGATTAC  | CTTCAGTAGT | 150  |
| TATGGCATGC | ACTGGGTCCG | CCAGGCTCCA | GGCAAGGGGC | TGGAGTGGGT | 200  |
| GGCAGTTATA | TGGTATGATG | GAAGCAATAA | ACACTATGCA | GACTCCGCGA | 250  |
| AGGGCCGATT | CACCATCTCC | AGAGACAATT | CCAAGAACAC | GCTGTATCTG | 300  |
| CAAATGAACA | GCCTGAGAGC | CGAGGACACG | GCTGTGTATT | ACTGTGCGAG | 350  |
| AGCCGGACTG | CTGGGTACT  | TTGACTACTG | GGGCCAGGGA | ACCCTGGTCA | 400  |
| CCGTCTCCTC | AGCCTCCACC | AAGGGCCCAT | CGGTCTTCCC | CCTGGCGCCC | 450  |
| TGCTCCAGGA | GCACCTCCGA | GAGCACAGCG | GCCCTGGGCT | GCCTGGTCAA | 500  |
| GGACTACTTC | CCCGAACCGG | TGACGGTGTC | GTGGAACCTA | GGCGCTCTGA | 550  |
| CCAGCGGCGT | GCACACCTTC | CCAGCTGTCC | TACAGTCCTC | AGGACTCTAC | 600  |
| TCCCTCAGCA | GCGTGGTGAC | CGTGCCCTCC | AGCAACTTCG | GCACCCAGAC | 650  |
| CTACACCTGC | AACGTAGATC | ACAAGCCCAG | CAACACCAAG | GTGGACAAGA | 700  |
| CAGTTGAGCG | CAAATGTTGT | GTCGAGTGCC | CACCGTGCCC | AGCACCACCT | 750  |
| GTGGCAGGAC | CGTCAGTCTT | CCTCTTCCCC | CCAAAACCCA | AGGACACCCT | 800  |
| CATGATCTCC | CGGACCCCTG | AGGTCACGTG | CGTGGTGGTG | GACGTGAGCC | 850  |
| ACGAAGACCC | CGAGGTCCAG | TTCAACTGGT | ACGTGGACGG | CGTGGAGGTG | 900  |
| CATAATGCCA | AGACAAAGCC | ACGGGAGGAG | CAGTTCAACA | GCACGTTCCG | 950  |
| TGTGGTCAGC | GTCCTCACCG | TTGTGCACCA | GGACTGGCTG | AACGGCAAGG | 1000 |
| AGTACAAGTG | CAAGGTCTCC | AACAAAGGCC | TCCAGCCCC  | CATCGAGAAA | 1050 |
| ACCATCTCCA | AAACCAAAGG | GCAGCCCCGA | GAACCACAGG | TGTACACCTT | 1100 |
| GCCCCCATCC | CGGGAGGAGA | TGACCAAGAA | CCAGGTCAGC | CTGACCTGCC | 1150 |
| TGGTCAAAGG | CTTCTACCCC | AGCGACATCG | CCGTGGAGTG | GGAGAGCAAT | 1200 |
| GGGCAGCCGG | AGAACAATA  | CAAGACCACA | CCTCCCATGC | TGGACTCCGA | 1250 |
| CGGCTCCTTC | TTCCTCTACA | GCAAGCTCAC | CGTGGACAAG | AGCAGGTGGC | 1300 |
| AGCAGGGGAA | CGTCTTCTCA | TGCTCCGTGA | TGCATGAGGC | TCTGCACAAC | 1350 |
| CACTACACGC | AGAAGAGCCT | CTCCCTGTCT | CCGGGTAAAT | GA         | 1392 |

(SEQ ID NO:30)

### 6.1.1 Heavy Chain Protein

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| MEFGLSWVFL | VALLRGVQCQ | VQLVESGGGV | VEPGRSLRLS | CTASGFTFSS | 50  |
| YGMHWVRQAP | GKGLEWVAVI | WYDGSNKHYA | DSAKGRFTIS | RDNSKNTLYL | 100 |
| QMNSLRAEDT | AVYYCARAGL | LGYFDYWQQG | TLVTVSSAST | KGPSVFPLAP | 150 |
| CSRSTSESTA | ALGCLVKDYF | PEPVTVSWNS | GALTSGVHTF | PAVLQSSGLY | 200 |
| SLSSVVTVPS | SNFGTQTYTC | NVDHKPSNTK | VDKTVERKCC | VECPPCPAPP | 250 |
| VAGPSVFLFP | PKPKDTLMIS | RTPEVTCVVV | DVSHEDPEVQ | FNWYVDGVEV | 300 |
| HNAKTKPREE | QFNSTFRVVS | VLTVVHQDWL | NGKEYKCKVS | NKGLPAPIEK | 350 |
| TISKTKGQPR | EPQVYTLPPS | REEMTKNQVS | LTCLVKGFYP | SDIAVEWESN | 400 |
| GQPENNYKTT | PPMLDSGGSF | FLYSKLTVDK | SRWQQGNVFS | CSVMHEALHN | 450 |
| HYTQKSLSL  | PGK        |            |            |            | 463 |

(SEQ ID NO:4)

**Figure 1D** (continued)**6.1.1 Kappa Chain DNA**

```

ATGGAAACCC CAGCGCAGCT TCTCTTCCTC CTGCTACTCT GGCTCCCAGA 50
TACCACCGGA GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT 100
CTCCAGGGGA AAGAGCCACC CTCTCCTGTA GGGCCAGTCA AAGTGTTAGC 150
AGCTACTTAG CCTGGTACCA ACAGAAACCT GGCCAGGCTC CCAGGCCCCCT 200
CATCTATGGT GTATCCAGCA GGGCCACTGG CATCCCAGAC AGGTTTCAGTG 250
GCAGTGGGTC TGGGACAGAC TTCACTCTCA CCATCAGCAG ACTGGAGCCT 300
GAAGATTTTG CAGTGTATTA CTGTCAGCAG TATGGTATCT CACCATTAC 350
TTTCGGCCCT GGGACCAAAG TGGATATCAA ACGAACTGTG GCTGCACCAT 400
CTGTCTTCAT CTTCCCGCCA TCTGATGAGC AGTTGAAATC TGGAAGTGCC 450
TCTGTTGTGT GCCTGCTGAA TAACTTCTAT CCCAGAGAGG CCAAAGTACA 500
GTGGAAGGTG GATAACGCCC TCCAATCGGG TAACTCCCAG GAGAGTGTCA 550
CAGAGCAGGA CAGCAAGGAC AGCACCTACA GCCTCAGCAG CACCCTGACG 600
CTGAGCAAAG CAGACTACGA GAAACACAAA GTCTACGCCT GCGAAGTCAC 650
CCATCAGGGC CTGAGCTCGC CCGTCACAAA GAGCTTCAAC AGGGGAGAGT 700
GTTAG 705

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(SEQ ID NO:43)

**6.1.1 Kappa Chain Protein**

```

METPAQLLFL LLLWLPDTTG EIVLTQSPGT LSLSPGERAT LSCRASQSVS 50
SYLAWYQQKP GQAPRPLIYG VSSRATGIPD RFSGSGSGTD FTLTISRLEP 100
EDFAVYYCQQ YGISPFTFGP GTKVDIKRTV AAPSVFIFPP SDEQLKSGTA 150
SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT 200
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC 234

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(SEQ ID NO:17)

**Figure 1E****3.1.1 Heavy Chain DNA**

```

GGCGTGGTCC AGCCTGGGAG GTCCCTGAGA CTCTCCTGTG CAGCGTCTGG 50
ATTCACCTTC AGTAGCTATG GCATGCACTG GGTCCGCCAG GCTCCAGGCA 100
AGGGGCTGGA GTGGGTGGCA GTTATATGGT ATGATGGAAG TAATAAATAC 150
TATGCAGACT CCGTGAAGGG CCGATTACAC ATCTCCAGAG ACAATTCCAA 200
GAACACGCTG TATCTGCAAA TGAACAGCCT GAGAGCCGAG GACACGGCTG 250
TGTATTACTG TGCGAGAGGG GCCCCGTATAA TAACCCCTTG TATGGACGTC 300
TGGGGCCAAG GGACCACGGT CACCGTCTCC TCAGCCTCCA CCAAGGGCCC 350
ATCGGTCTTC CCCCTGGCGC CCTGCTCCAG GAGCACCTCC GAGAGCACAG 400
CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 450
TCGTGGAAC T CAGGCGCTCT GACCAGCGGC GTGCACACCT TCCCAGCTGT 500
CCTACAG 507

```

(SEQ ID NO:31)

**3.1.1 Heavy Chain Protein**

```

GVVQPGRSLR LSCAASGFTF SSYGMHWVRQ APGKGLEWVA VIWYDGSNKY 50
YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCARG ARIITPCMDV 100
WGQGTIVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV 150
SWNSGALTSG VHTFPAVLQ 169

```

(SEQ ID NO:5)

**3.1.1 Kappa Chain DNA**

```

CAGTCTCCAT CCTCCCTGTC TGCATCTGTA GGAGACAGAG TCACCATCAC 50
TTGCCGGGCA AGTCAGAGCA TTAACACCTA TTTAATTTGG TATCAGCAGA 100
AACCAGGGAA AGCCCCTAAC TTCCTGATCT CTGCTACATC CATTTTGCAA 150
AGTGGGGTCC CATCAAGGTT CCGTGGCAGT GGCTCTGGGA CAAATTTTCAC 200
TCTCACCATC AACAGTCTTC ATCCTGAAGA TTTTGCAACT TACTACTGTC 250
AACAGAGTTA CAGTACCCCA TTCACTTTTCG GCCCTGGGAC CAAAGTGGAT 300
ATCAAACGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA 350
TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT 400
TCTATCCCAG AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA 450
TCGGGTAA 458

```

(SEQ ID NO:44)

**3.1.1 Kappa Chain Protein**

```

QSPSSLSASV GDRVITICRA SQSINTYLIW YQQKPGKAPN FLISATSIHQ 50
SGVPSRFRGS GSGTNFTLTI NSLHPEDFAT YYCQQSYSTP FTFGPGTKVD 100
IKRTVAAPSV FIFPPSDEQL KSGTASVCL LNNFYPREAK VQWKVDNALQ 150
SG 152

```

(SEQ ID NO:18)



**Figure 1F****4.10.2 Heavy Chain DNA**

```

GGCGTGGTCC AGCCTGGGAG GTCCCTGAGA CTCTCCTGTG TAGCGTCTGG 50
ATTCATCTTC AGTAGTCATG GCATCCACTG GGTCCGCCAG GCTCCAGGCA 100
AGGGGCTGGA GTGGGTGGCA GTTATATGGT ATGATGGAAG AAATAAAGAC 150
TATGCAGACT CCGTGAAGGG CCGATTACAC ATCTCCAGAG ACAATTCCAA 200
GAACACGCTG TATTTGCAAA TGAACAGCCT GAGAGCCGAG GACACGGCTG 250
TGTATTACTG TGCGAGAGTG GCCCCACTGG GGCCACTTGA CTA CTACTGGGGC 300
CAGGGAACCC TGGTCACCGT CTCCTCAGCC TCCACCAAGG GCCCATCGGT 350
CTTCCCCCTG GCGCCCTGCT CCAGGAGCAC CTCCGAGAGC ACAGCGGCCC 400
TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 450
AACTCAGGCG CTCTGACCAG CGGCGTGCAC ACCTTCCCAG CTGTCCTACA 500
G 501

```

(SEQ ID NO:32)

**4.10.2 Heavy Chain Protein**

```

GVVQPGRSLR LSCVASGFIF SSHGIHWVRQ APGKGLEWVA VIWYDGRNKD 50
YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCARV APLGPLDYWG 100
QGTLVTVSSA STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTVSW 150
NSGALTSGVH TFPVLQ 167

```

(SEQ ID NO:6)

**4.10.2 Kappa Chain DNA**

```

TCTCCAGGCA CCCTGTCTTT GTCTCCAGGG GAAAGAGCCA CCCTCTCCTG 50
CAGGGCCAGT CAGAGTATTA GCAGCAATTT CTTAGCCTGG TACCAGCAGA 100
AACCTGGCCA GGCTCCAGG CTCCTCATCT ATCGTCCATC CAGCAGGGCC 150
ACTGGCATCC CAGACAGTTT CAGTGGCAGT GGGTCTGGGA CAGACTTCAC 200
TCTCACCATC AGCAGACTGG AGCCTGAGGA TTTTGCATTA TATTACTGTC 250
AGCAGTATGG TACGTCACCA TTCACTTTCG GCCCTGGGAC CAAAGTGGAT 300
ATCAAGCGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA 350
TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT 400
TCTATCCCAG AGAGGCCAAA GTACAG 426

```

(SEQ ID NO:45)

**4.10.2 Kappa Chain Protein**

```

SPGTLSSLSPG ERATLSCRAS QSISSNFLAW YQKPGQAPR LLIYRPSSRA 50
TGIPDSFSGS GSGTDFTLTI SRLEPEDFAL YYCQYGTSP FTFGPGTKVD 100
IKRTVAAPSV FIFPPSDEQL KSGTASVACL LNNFYPREAK VQ 142

```

(SEQ ID NO:19)

**Figure 1G****2.1.3 Heavy Chain DNA**

```

TCGGGCCCAG GACTGGTGAA GCCTTCACAG ATCCTGTCCC TCACCTGCAC 50
TGTCTCTGGT GGCTCCATCA GCAGTGGTGG TCACTACTGG AGCTGGATCC 100
GCCAGCACCC AGGGAAGGGC CTGGAGTGGG TTGGGTACAT CTATTACATT 150
GGGAACACCT ACTACAACCC GTCCCTCAAG AGTCGAGTTA CCATATCAGT 200
AGACACGTCT AAGAACCAGT TCTCCCTGAA GCTGAGCTCT GTGACTGCCG 250
CGGACACGGC CGTGTATTAT TGTGCGAGAG ATAGTGGGGA CTACTACGGT 300
ATAGACGTCT GGGGCCAAGG GACCACGGTC ACCGTCTCCT CAGCTTCCAC 350
CAAGGGCCCA TCCGTCTTCC CCCTGGCGCC CTGCTCCAGG AGCACCTCCG 400
AGAGCACAGC CGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCCGAACCG 450
GTGACGGTGT CGTGGAAGTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT 500
CCCGGCTGTC CTACAA 516

```

(SEQ ID NO:33)

**2.1.3 Heavy Chain Protein**

```

SGPGLVKPSQ ILSLTCTVSG GSISGGHYW SWIRQHPGKG LEWIGYIYYI 50
GNTYYNPSLK SRVTISVDTS KNQFSLKLSS VTAADTAVYY CARDSGDYYG 100
IDVWGQGT TVSSASTKGP SVFPLAPCSR STSESTAALG CLVKDYFPEP 150
VTVSWNSGAL TSGVHTFPAV LQ 172

```

(SEQ ID NO:7)

**2.1.3 Kappa Chain DNA**

```

TCTCCAGACT TTCAGTCTGT GACTCCAAAG GAGAAAGTCA CCATCACCTG 50
CCGGGCCAGT CAGAGCATTG GTAGTAGCTT ACATTGGTAT CAGCAGAAAC 100
CAGATCAGTC TCCAAAGCTC CTCATCAAGT ATGCTTCCCA GTCCTTCTCT 150
GGGGTCCCCT CGAGGTTTCAG TGGCAGTGGG TCTGGGACAG ATTTACCCT 200
CACCATCAAT AGCCTGGAAG CTGAAGATGC TGCAACGTAT TACTGTCATC 250
AGAGTAGTAG TTTACCGCTC ACTTTCGGCG GAGGGACCAA GGTGGAGATC 300
AAACGAACTG TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA 350
GCAGTTGAAA TCTGGAAGTC CCTCTGTTGT GTGCCTGCTG AATAACTTCT 400
ATCCCAGAGA GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG 450
GGTAACTCCC AGGAG 465

```

(SEQ ID NO:46)

**2.1.3 Kappa Chain Protein**

```

SPDFQSVTPK EKVTITCRAS QSIGSSLHWY QQKPDQSPKL LIKYASQSFS 50
GVPSRFGSGS SGTDFTLTIN SLEAEDAATY YCHQSSSLPL TFGGGTKVEI 100
KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREKQV QWKVDNALQS 150
GNSQE 155

```

(SEQ ID NO:20)

**Figure 1H****4.13.1 Heavy Chain DNA**

```

CCTGGGAGGT CCCTGAGACT CTCCTGTGCA GCGTCTGGAT TCACCTTCAG 50
TAGTCATGGC ATCCACTGGG TCCGCCAGGC TCCAGGCAAG GGGCTGGAGT 100
GGGTGGCAGT TATATGGTAT GATGGAAGAA ATAAAGACTA TGCAGACTCC 150
GTGAAGGGCC GATTCACCAT CTCCAGAGAC AATTCCAAGA ACACGCTGTA 200
TTTGCAAATG AACAGCCTGA GAGCCGAGGA CACGGCTGTG TATTACTGTG 250
CGAGAGTGGC CCCACTGGGG CCACTTGACT ACTGGGGCCA GGAACCCCTG 300
GTCACCGTCT CCTCAGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 350
GCCCTGCTCC AGGAGCACCT CCGAGAGCAC AGCGGCCCTG GGCTGCCTGG 400
TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCT 450
CTGACCAGC 459

```

(SEQ ID NO:34)

**4.13.1 Heavy Chain Protein**

```

PGRSLRLSCA ASGFTFSSHG IHWVRQAPGK GLEWVAVIWY DGRNKDYADS 50
VKGRFTISR D NSKNTLYLQM NSLRAEDTAV YYCARVAPLG PLDYWGQGT 100
LTS
VTVSSASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA 150
153

```

(SEQ ID NO:8)

**4.13.1 Kappa Chain DNA**

```

CAGTCTCCAG GCACCCTGTC TTTGTCTCCA GGGGAAAGAG CCACCCTCTC 50
CTGCAGGGCC AGTCAGAGTG TCAGCAGCTA CTTAGCCTGG TACCAGCAGA 100
AACCTGGCCA GGCTCCCAGG CTCCTCATCT ATGGTGCATC CAGCAGGGCC 150
ACTGGCATCC CAGACAGGTT CAGTGGCAGT GGGTCTGGGA CAGACTTCAC 200
TCTCACCATC AGCAGACTGG AGCCTGAGGA TTTTGCAGTG TATTACTGTC 250
AACAGTATGG TAGGTCACCA TTTCACTTTTCG GCCCTGGGAC CAAAGTAGAT 300
ATCAAGCGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA 350
TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT 400
TCTATCCAG AGAGGCCAAA GTACAGTGGA AAGGTGGATA 440

```

(SEQ ID NO:47)

**4.13.1 Kappa Chain Protein**

```

QSPGTL LSLSP GERATLSCRA SQSVSSYLAW YQKPGQAPR LLIYGASSRA 50
TGIPDRFSGS GSGTDFTLTI SRLEPEDFAV YYCQYGRSP FTFGPGTKVD 100
IKRTVAAPSV FIFPPSDEQL KSGTASVCL LNNFYPREAK VQWKGG 146

```

(SEQ ID NO:21)

**Figure 11****11.2.1 Heavy Chain DNA**

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| GGCGTGGTCC | AGCCTGGGAG | GTCCCTGAGA | CTCTCCTGTG | CAGCGTCTGG | 50  |
| ATTCACCTTC | AGTAGCTATG | GCATGCACTG | GGTCCGCCAG | GCTCCAGGCA | 100 |
| AGGGGCTGGA | GTGGGTGGCA | GTTATATGGT | ATGATGGAAG | TAATAAATAC | 150 |
| TATGCAGACT | CCGTGAAGGG | CCGATTACAC | ATCTCCAGAG | ACAATTCCAA | 200 |
| GAACACGCTG | TATCTGCAAA | TGAACAGCCT | GAGAGCCGAG | GACACGGCTG | 250 |
| TGTATTACTG | TGCGAGAGAT | CCGAGGGGAG | CTACCCTTTA | CTACTACTAC | 300 |
| TACCGGTKGG | ACGTCTGGGG | CCAAGGGACC | ACGGTCACCG | TCTCCTCAGC | 350 |
| CTCCACCAAG | GGCCCATCGG | TCTTCCCCCT | GGCGCCCTGC | TCCAGGAGCA | 400 |
| CCTCCGAGAG | CACAGCGGCC | CTGGGCTGCC | TGGTCAAGGA | CTACTTCCCC | 450 |
| GAACCGGTGA | CGGTGTCGTG | GAATCAGGC  | GCTCTGACCA | GCGGCGTGCA | 500 |
| CAC        |            |            |            |            | 503 |

(SEQ ID NO:35)

**11.2.1 Heavy Chain Protein**

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| GVVQPGRSLR | LSCAASGFTF | SSYGMHWVRQ | APKGLEWVA  | VIWYDGSNKY | 50  |
| YADSVKGRFT | ISRDNKNL   | YLMNSLRAE  | DTAVYYCARD | PRGATLYYYY | 100 |
| YRXDVWGQGT | TVTVSSASTK | GPSVFPLAPC | SRSTSESTAA | LGCLVKDYFP | 150 |
| EPVTVSWNSG | ALTSGVH    |            |            |            | 167 |

(SEQ ID NO:9)

**11.2.1 Kappa Chain DNA**

|            |             |            |            |            |     |
|------------|-------------|------------|------------|------------|-----|
| CCATCCTCCC | TGTCTGCATC  | TGTAGGAGAC | AGAGTCACCA | TCACTTGCCG | 50  |
| GGCAAGTCAG | AGCATTAAACA | GCTATTTAGA | TTGGTATCAG | CAGAAACCAG | 100 |
| GGAAAGCCCC | TAAACTCCTG  | ATCTATGCTG | CATCCAGTTT | GCAAAGTGGG | 150 |
| GTCCCATCAA | GGTTCAGTGG  | CAGTGGATCT | GGGACAGATT | TCACTCTCAC | 200 |
| CATCAGCAGT | CTGCAACCTG  | AAGATTTTGC | AACTTACTAC | TGTCAACAGT | 250 |
| ATTACAGTAC | TCCATTCACT  | TTCGGCCCTG | GGACCAAAGT | GGAAATCAAA | 300 |
| CGAACTGTGG | CTGCACCATC  | TGTCTTCATC | TTCCCGCCAT | CTGATGAGCA | 350 |
| GTTGAAATCT | GGAAGTGCCT  | CTGTTGTGTG | CCTGCTGAAT | AACTTCTATC | 400 |
| CCAGAGAGGC | CAAAGTA     |            |            |            | 417 |

(SEQ ID NO:48)

**11.2.1 Kappa Chain Protein**

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| PSSLASVGD  | RVTITCRASQ | SINSYLDWYQ | QKPGKAPKLL | IYAASSLQSG | 50  |
| VPSRFSGSGS | GTDFTLTIS  | LQPEDFATYY | CQYYSTPFT  | FGPGTKVEIK | 100 |
| RTVAAPSVFI | FPPSDEQLKS | GTASVVCLLN | NFYPREAKV  |            | 139 |

(SEQ ID NO:22)

**Figure 1J****11.6.1 Heavy Chain DNA**

```

GGCGTGGTCC AGCCTGGGAG GTCCCTGAGA CTCTCCTGTG CAGCGTCTGG 50
ATTCACCTTC AGTAGCTATG GCATGCACTG GGTCCGCCAG GCTCCAGGCA 100
AGGGGCTGGA GTGGGTGGCA GTTATATGGT ATGATGGAAG TCATAAATAC 150
TATGCAGACT CCGTGAAGGG CCGATTACAC ATCTCCAGAG ACAATTCCAA 200
GAACACGCTG TATCTGCAAA TGAACAGCCT GAGAGCCGAG GACACGGCTG 250
TGTATTACTG TGCAGAGAGG GCTGTAGTAG TACCAGCTGC TATGGACGTC 300
TGGGGCCAAG GGACCACGGT CACCGTCTCC TCAGCCTCCA CCAAGGGCCC 350
ATCGGTCTTC CCCCTGGCGC CCTGCTCCAG GAGCACCTCC GAGAGCACAG 400
CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 450
T                                                                 451

```

(SEQ ID NO:36)

**11.6.1 Heavy Chain Protein**

```

GVVQPGRSLR LSAAAGSFTF SSYGMHWVRQ APGKGLEWVA VIWYDGS HKY 50
YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCARG AVVVPAAMDV 100
WGQGT TVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV 150
S                                                                 151

```

(SEQ ID NO:10)

**11.6.1 Kappa Chain DNA**

```

ACCCAGTCTC CATCCTCCCT GTCTGCATCT GTAGGAGACA GAGTCACCAT 50
CACTTGCCGG GCAAGTCAGA ACATTAGCAG GTATTTAAAT TGGTATCAAC 100
AGAAACCAGG GAAAGCCCCT AAGTTCCTGA TCTATGTTGC ATCTATTTTG 150
CAAAGTGGGG TCCCATCAGG GTTCAGTGCC AGTGGATCTG GGCCAGATTT 200
CACTCTNACC ATCAGCAGTC TGCAACCTGA AGATTTTGCA ACTTACTACT 250
GTCAACAGAG TTACAGTACC CCATTCACTT TCGGCCCTGG GACCAAAGTG 300
GATATCAAAC GAACTGTGGC TGCACCATCT GTCTTCATCT TCCCGCCATC 350
TGATGAGCAG TTGAAATCTG GAACTGCCTC TGTTGTGTGC CTGCTGAATA 400
AC                                                                 402

```

(SEQ ID NO:49)

**11.6.1 Kappa Chain Protein**

```

TQSPSSLSAS VGDRVITICR ASQNISRYLN WYQQKPGKAP KFLIYVASIL 50
QSGVPSGFS SSGSPDFTLT ISSLQPEDFA TYQCQSYST PFTFGPGTKV 100
DIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNN 134

```

(SEQ ID NO:23)

**Figure 1K****11.7.1 Heavy Chain DNA**

```

GTGGTCCAGC CTGGGAGGTC CCTGAGACTC TCCTGTGCAG CGTCTGGATT 50
CACCTTCAGT AGCNGTGGCA TGCCTGGGT CCGCCAGGCT CCAGGCAAGG 100
GGCTGGAGTG GGTGGCAGTT ATATGGTCTG ATGGAAGTCA TAAATACTAT 150
GCAGACTCCG TGAAGGGCCG ATTCACCATC TCCAGAGACA ATTCCAAGAA 200
CACGCTGTAT CTGCAAATGA ACAGCCTGAG AGCCGAGGAC ACGGCTGTGT 250
ATTACTGTGC GAGAGGAACT ATGATAGTAG TGGGTACCCT TGACTACTGG 300
GGCCAGGGAA CCCTGGTCAC CGTCTCCTCA GCCTCCACCA AGGGCCCATC 350
GGTCTTCCCC CTGGCGCCCT GCTCCAGGAG CACCTCCGAG AGCACAGCGG 400
CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCG 438

```

(SEQ ID NO:37)

**11.7.1 Heavy Chain Protein**

```

VVQPGRSLRL SCAASGFTFS SXGMHWVRQA PGKGLEWVAV IWSDGSHKYY 50
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARGT MIVVGTLDYW 100
QGQTLVTVSS ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEP 146

```

(SEQ ID NO:11)

**11.7.1 Kappa Chain DNA**

```

ACCCAGTCTC CATCCTCCCT GTCTGCATCT GTAGGAGACA GAGTCACCAT 50
CACTTGCCGG GCAAGTCAGA GCATTTGCAA CTATTTAAAT TGGTATCAGC 100
AGAAACCAGG AAAAGCCCCT AGGGTCCTGA TCTATGCTGC ATCCAGTTTG 150
CAAGGTGGGG TCCCGTCAAG GTTCAGTGGC AGTGGATCTG GGACAGATTG 200
CACTCTCACC ATCAGCAGTC TGCAACCTGA AGATTTTGCA ACTTACTACT 250
GTCAACAGAG TTACACTACC CCATTCACTT TCGGCCCTGG GACCAGAGTG 300
GATATCGAAC GAACTGTGGC TGCACCATCT GTCTTCATCT TCCCGCCATC 350
TGATGAGCAG TTGAAATCTG GAACTGCCTC TGTGTGTGTC CTGCTGAATA 400
ACTTCTATCC CAGAGAGGCC AAAGTACAGT GGAAGGTGGA TAACGCCTAT 450
T 451

```

(SEQ ID NO:50)

**11.7.1 Kappa Chain Protein**

```

TQSPSSLSAS VGDRVITITCR ASQSICNYLN WYQQKPGKAP RVLIIYAASSL 50
QGGVPSRFSG SGSGIDCTLT ISSLQPEDFA TYQCQSYIT PFTFGPGTRV 100
DIERTVAAPS VFIFPPSDEQ LKSGTASVVC LLNMFYPREA KVQWKVDNAY 150

```

(SEQ ID NO:24)

**Figure 1L****12.3.1.1 Heavy Chain DNA**

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TCCTGTGCAG | CGTCTGGATT | CACCTTCAGT | TACTATGGCG | TCTGGGGGAG | 50  |
| GCGTGGTCCA | GCCTGGGAGG | TCCCTGAGAC | TCTCCTGTGC | AGCGTCTGGA | 100 |
| TTCACCTTCA | GTAGCTATGG | CGTGCACCTG | GTCCGCCAGG | CTCCAGGCAA | 150 |
| GGGGCTGGAG | TGGGTGGCAG | TTATATGGTA | TGATGGAAGT | AATAAATACT | 200 |
| ATGCAGACTC | CGTGAAGGGC | CGATTACCA  | TCTCCAGAGA | CAATTCCAAG | 250 |
| AGCACGCTGT | ATCTGCAAAT | GAACAGCCTG | AGAGCCGAGG | ACACGGCTGT | 300 |
| GTATTATTGT | GCGAGAGACT | CGTATTACGA | TTTTTGGAGT | GGTCGGGGCG | 350 |
| GTATGGACGT | CTGGGGCCAA | GGGACCACGG | TCACCGTCTC | CTCAGCCTCC | 400 |
| ACCAAGGGCC | CATCGGTCTT | CCCCCTGGCG | CCCTGCTCCA | GGAGCACCTC | 450 |
| CGAGAGCACA | GCGGCCCTGG | GCTGCCTGGT | CAAGGACTAC | TTCCCCGAAC | 500 |
| CGGTGACGGT | GTCGTGGAAC | TCAGGCGCTC | TGACCAGCGG | CGTGCACACC | 550 |
| TTCCAGCTG  | TC         |            |            |            | 562 |

(SEQ ID NO:38)

**12.3.1.1 Heavy Chain Protein**

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| SGGGVVQPGR | SLRLSCAASG | FTFSSYGVHW | VRQAPGKGLE | WVAVIWDGS  | 50  |
| NKYYADSVKG | RFTISRDNSK | STLYLQMNSL | RAEDTAVYYC | ARDSYYDFWS | 100 |
| GRGMDVWGQ  | GTTVTVSSAS | TKGPSVFPLA | PCSRSTSEST | AALGCLVKDY | 150 |
| FPEPVTVSWN | SGALTSGVHT | FPAV       |            |            | 174 |

(SEQ ID NO:12)

**12.3.1.1 Kappa Chain DNA**

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CCACTCTCCC | TGCCCCTCAC | CCTTGGACAG | CCGGCCTCCA | TCTCCTGCAG | 50  |
| GTCTAGTCAA | AGCCTCGTAT | ACAGTGATGG | AAACACCTAC | TTGAATTGGT | 100 |
| TTCAGCAGAG | GCCAGGCCAA | TCTCCAAGGC | GCCTAATTTA | TAAGGTTTCT | 150 |
| AACTGGGACT | CTGGGGTCCC | AGACAGATTC | AGCGGCAGTG | GGTCAGGCAC | 200 |
| TGATTTTACA | CTGAAAATCA | GCAGGGTGGA | GGCTGAGGAT | GTTGGGGTTT | 250 |
| ATTACTGCAT | GCAAGGTTCA | CACTGGCCTC | CGACGTTTCG | CCAAGGGACC | 300 |
| AAGGTGGA   | TCAAACGAAC | TGTGGCTGCA | CCATCTGTCT | TCATCTTCCC | 350 |
| GCCATCTGAT | GAGCAGTTGA | AATCTGGAAC | TGCCTCTGTT | GTGTGCCTGC | 400 |
| TGAATAACTT | CTATCCCAC  |            |            |            | 419 |

(SEQ ID NO:51)

**12.3.1.1 Kappa Chain Protein**

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| PLSLPVTLGQ | PASISCRSSQ | SLVYSDGNTY | LNWFQQRPGQ | SPRRLIYKVS | 50  |
| NWDSGVPDRF | SGSGSGTDFT | LKISRVEAED | VGVIYCMQGS | HWPPTFGQGT | 100 |
| KVEIKRTVAA | PSVFIFPPSD | EQLKSGTASV | VCLLNNFYP  |            | 139 |

(SEQ ID NO:25)

**Figure 1M****12.9.1.1 Heavy Chain DNA**

```

GTCCAGCCTG GGAGGTCCCT GAGACTCTCC TGTGCAGCGT CTGGATTAC 50
CTTCAGTAAC TATGCCATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC 100
TGGAGTGGGT GGTAGTTATT TGGCATGATG GAAATAATAA ATACTATGCA 150
GAGTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATT CCAAGAACAC 200
GCTGTATCTG CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTATATT 250
ACTGTGCGAG AGATCAGGGC ACTGGCTGGT ACGGAGGCTT TGACTTCTGG 300
GGCCAGGGAA CCCTGGTCAC CGTCTCCTCA GCCTCCACCA AGGGCCCATC 350
GGTCTTCCCC CTGGCGCCCT GCTCCAGGAG CACCTCCGAG AGCACAGCGG 400
CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG 450
TGGAACTCAG GCGCTCTGAC CAGCGGCGTG CACACCTTCC 490

```

(SEQ ID NO:39)

**12.9.1.1 Heavy Chain Protein**

```

VQPGRSLRLS CAASGFTFSN YAMHWVRQAP GKGLEWVVVI WHDGNNKYIA 50
ESVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCARDQG TGWYGGFDFW 100
GQGTLVTVSS ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS 150
WNSGALTSGV HTF 163

```

(SEQ ID NO:13)

**12.9.1.1 Kappa Chain DNA**

```

CCTGGAGAGC CGGCTTCCAT CTCTTGCAGG TCTAGTCAGA GCCTCCTGCA 50
TAGTAATGGA TACAACTATT TGGATTGGTA CCTGCAGAAG CCAGGACAGT 100
CTCCACAGCT CCTGATCTAT TTGGGTCTTA ATCGGGCCTC CGGGGTCCCT 150
GACAGGTTCA GTGGCAGTGG ATCAGGCACA GATTTTACAC TGAAACTCAG 200
CAGAGTGGAG GCTGAGGATG TTGGGGTTTA TTA CTGCATG CAAGCTCTAC 250
AAACTCCTCT CACTTTCGGC GGAGGGACCA AGGTGGAGAT CAAACGAACT 300
GTGGCTGCAC CATCTGTCTT CATCTTCCCG CCATCTGATG AGCAGTTGAA 350
ATCTGGAAC TGCCTCTGTTG TGTGCCTGCT GAATAACTTC TATCCCAGAR 400
AGGCCAAAGT ACATTCCAT 419

```

(SEQ ID NO:52)

**12.9.1.1 Kappa Chain Protein**

```

PGEPAISCR SSQSLLSNG YNYLDWYLQK PGQSPQLLIY LGSNRASGVP 50
DRFSGSGSGT DFTLKL SRVE AEDVG VYYCM QALQTPLTFG GGTKVEIKRT 100
VAAPSVFIFP PSDEQLKSGT ASVVC LLN NF YPR 133

```

(SEQ ID NO:26)



**Figure 2A**

| CDR  | DP5<br>0 | 3.1.1 | 4.1.1 | 4.8.1 | 4.10.<br>2 | 4.13.<br>1 | 4.14.<br>3 | 6.1.1 | 11.2.<br>1 | 11.6.<br>1 | 11.7.<br>1 | 12.3.<br>1.1 | 12.9.<br>1.1 |
|------|----------|-------|-------|-------|------------|------------|------------|-------|------------|------------|------------|--------------|--------------|
|      |          |       |       |       |            |            |            | G     |            |            |            |              |              |
|      | G        | G     | G     | G     | G          |            |            | G     | G          | G          |            | G            |              |
|      | V        | V     | V     | V     | V          |            |            | V     | V          | V          | V          | V            |              |
|      | V        | V     | V     | V     | V          |            |            | V     | V          | V          | V          | V            | V            |
|      | Q        | Q     | Q     | Q     | Q          |            |            | E     | Q          | Q          | Q          | Q            | Q            |
|      | P        | P     | P     | P     | P          | P          | P          | P     | P          | P          | P          | P            | P            |
|      | G        | G     | G     | G     | G          | G          | G          | G     | G          | G          | G          | G            | G            |
|      | R        | R     | R     | R     | R          | R          | R          | R     | R          | R          | R          | R            | R            |
|      | S        | S     | S     | S     | S          | S          | S          | S     | S          | S          | S          | S            | S            |
|      | L        | L     | L     | L     | L          | L          | L          | L     | L          | L          | L          | L            | L            |
|      | R        | R     | R     | R     | R          | R          | R          | R     | R          | R          | R          | R            | R            |
|      | L        | L     | L     | L     | L          | L          | L          | L     | L          | L          | L          | L            | L            |
|      | S        | S     | S     | S     | S          | S          | S          | S     | S          | S          | S          | S            | S            |
|      | C        | C     | C     | C     | C          | C          | C          | C     | C          | C          | C          | C            | C            |
|      | A        | A     | V     | T     | V          | A          | A          | T     | A          | A          | A          | A            | A            |
|      | A        | A     | A     | A     | A          | A          | A          | A     | A          | A          | A          | A            | A            |
|      | S        | S     | S     | S     | S          | S          | S          | S     | S          | S          | S          | S            | S            |
|      | G        | G     | G     | G     | G          | G          | G          | G     | G          | G          | G          | G            | G            |
|      | F        | F     | F     | F     | F          | F          | F          | F     | F          | F          | F          | F            | F            |
|      | T        | T     | T     | T     | I          | T          | T          | T     | T          | T          | T          | T            | T            |
|      | F        | F     | F     | F     | F          | F          | F          | F     | F          | F          | F          | F            | F            |
| CDR1 | S        | S     | S     | S     | S          | S          | S          | S     | S          | S          | S          | S            | S            |
|      | S        | S     | S     | N     | S          | S          | S          | S     | S          | S          | S          | S            | N            |
|      | Y        | Y     | H     | Y     | H          | H          | H          | Y     | Y          | Y          | C          | Y            | Y            |
|      | G        | G     | G     | G     | G          | G          | G          | G     | G          | G          | G          | G            | A            |
|      | M        | M     | M     | M     | I          | I          | I          | M     | M          | M          | M          | V            | M            |
|      | H        | H     | H     | H     | H          | H          | H          | H     | H          | H          | H          | H            | H            |
|      | W        | W     | W     | W     | W          | W          | W          | W     | W          | W          | W          | W            | W            |
|      | V        | V     | V     | V     | V          | V          | V          | V     | V          | V          | V          | V            | V            |
|      | R        | R     | R     | R     | R          | R          | R          | R     | R          | R          | R          | R            | R            |
|      | Q        | Q     | Q     | Q     | Q          | Q          | Q          | Q     | Q          | Q          | Q          | Q            | Q            |
|      | A        | A     | A     | A     | A          | A          | A          | A     | A          | A          | A          | A            | A            |
|      | P        | P     | P     | P     | P          | P          | P          | P     | P          | P          | P          | P            | P            |
|      | G        | G     | G     | G     | G          | G          | G          | G     | G          | G          | G          | G            | G            |
|      | K        | K     | K     | K     | K          | K          | K          | K     | K          | K          | K          | K            | K            |
|      | G        | G     | G     | G     | G          | G          | G          | G     | G          | G          | G          | G            | G            |
|      | L        | L     | L     | L     | L          | L          | L          | L     | L          | L          | L          | L            | L            |
|      | E        | E     | E     | E     | E          | E          | E          | E     | E          | E          | E          | E            | E            |
|      | W        | W     | W     | W     | W          | W          | W          | W     | W          | W          | W          | W            | W            |
|      | V        | V     | V     | V     | V          | V          | V          | V     | V          | V          | V          | V            | V            |
|      | A        | A     | A     | A     | A          | A          | A          | A     | A          | A          | A          | A            | V            |
|      | V        | V     | V     | V     | V          | V          | V          | V     | V          | V          | V          | V            | V            |
|      | I        | I     | I     | I     | I          | I          | I          | I     | I          | I          | I          | I            | I            |
|      | W        | W     | W     | W     | W          | W          | W          | W     | W          | W          | W          | W            | W            |
|      | Y        | Y     | Y     | Y     | Y          | Y          | Y          | Y     | Y          | Y          | S          | Y            | H            |
|      | D        | D     | D     | D     | D          | D          | D          | D     | D          | D          | D          | D            | D            |
|      | G        | G     | G     | G     | G          | G          | G          | G     | G          | G          | G          | G            | G            |
| CDR2 | S        | S     | R     | S     | R          | R          | R          | S     | S          | S          | S          | S            | N            |

**Figure 2B**

| CDR  | DP5<br>0 | 3.1.1 | 4.1.1 | 4.8.1 | 4.10.<br>2 | 4.13.<br>1 | 4.14.<br>3 | 6.1.1 | 11.2.<br>1 | 11.6.<br>1 | 11.7.<br>1 | 12.3.<br>1.1 | 12.9.<br>1.1 |
|------|----------|-------|-------|-------|------------|------------|------------|-------|------------|------------|------------|--------------|--------------|
|      | N        | N     | N     | N     | N          | N          | N          | N     | N          | H          | H          | N            | N            |
|      | K        | K     | K     | K     | K          | K          | K          | K     | K          | K          | K          | K            | K            |
|      | Y        | Y     | Y     | H     | D          | D          | D          | H     | Y          | Y          | Y          | Y            | Y            |
|      | Y        | Y     | Y     | Y     | Y          | Y          | Y          | Y     | Y          | Y          | Y          | Y            | Y            |
|      | A        | A     | A     | G     | A          | A          | A          | A     | A          | A          | A          | A            | A            |
|      | D        | D     | D     | D     | D          | D          | D          | D     | D          | D          | D          | D            | E            |
|      | S        | S     | S     | S     | S          | S          | S          | S     | S          | S          | S          | S            | S            |
|      | V        | V     | V     | V     | V          | V          | V          | A     | V          | V          | V          | V            | V            |
|      | K        | K     | K     | K     | K          | K          | K          | K     | K          | K          | K          | K            | K            |
|      | G        | G     | G     | G     | G          | G          | G          | G     | G          | G          | G          | G            | G            |
|      | R        | R     | R     | R     | R          | R          | R          | R     | R          | R          | R          | R            | R            |
|      | F        | F     | F     | F     | F          | F          | F          | F     | F          | F          | F          | F            | F            |
|      | T        | T     | T     | T     | T          | T          | T          | T     | T          | T          | T          | T            | T            |
|      | I        | I     | I     | I     | I          | I          | I          | I     | I          | I          | I          | I            | I            |
|      | S        | S     | S     | S     | S          | S          | S          | S     | S          | S          | S          | S            | S            |
|      | R        | R     | R     | S     | R          | R          | R          | R     | R          | R          | R          | R            | R            |
|      | D        | D     | D     | D     | D          | D          | D          | D     | D          | D          | D          | D            | D            |
|      | N        | N     | N     | N     | N          | N          | N          | N     | N          | N          | N          | N            | N            |
|      | S        | S     | S     | S     | S          | S          | S          | S     | S          | S          | S          | S            | S            |
|      | K        | K     | K     | K     | K          | K          | K          | K     | K          | K          | K          | K            | K            |
|      | N        | N     | N     | N     | N          | N          | K          | N     | N          | N          | N          | S            | N            |
|      | T        | T     | T     | T     | T          | T          | T          | T     | T          | T          | T          | T            | T            |
|      | L        | L     | L     | L     | L          | L          | L          | L     | L          | L          | L          | L            | L            |
|      | Y        | Y     | F     | Y     | Y          | Y          | Y          | Y     | Y          | Y          | Y          | Y            | Y            |
|      | L        | L     | L     | L     | L          | L          | L          | L     | L          | L          | L          | L            | L            |
|      | Q        | Q     | Q     | Q     | Q          | Q          | Q          | Q     | Q          | Q          | Q          | Q            | Q            |
|      | M        | M     | M     | M     | M          | M          | M          | M     | M          | M          | M          | M            | M            |
|      | N        | N     | N     | N     | N          | N          | N          | N     | N          | N          | N          | N            | N            |
|      | S        | S     | S     | S     | S          | S          | S          | S     | S          | S          | S          | S            | S            |
|      | L        | L     | L     | L     | L          | L          | L          | L     | L          | L          | L          | L            | L            |
|      | R        | R     | R     | R     | R          | R          | R          | R     | R          | R          | R          | R            | R            |
|      | A        | A     | A     | A     | A          | A          | A          | A     | A          | A          | A          | A            | A            |
|      | E        | E     | E     | E     | E          | E          | E          | E     | E          | E          | E          | E            | E            |
|      | D        | D     | D     | D     | D          | D          | D          | D     | D          | D          | D          | D            | D            |
|      | T        | T     | T     | T     | T          | T          | T          | T     | T          | T          | T          | T            | T            |
|      | A        | A     | A     | A     | A          | A          | A          | A     | A          | A          | A          | A            | A            |
|      | V        | V     | V     | V     | V          | V          | V          | V     | V          | V          | V          | V            | V            |
|      | Y        | Y     | Y     | Y     | Y          | Y          | Y          | Y     | Y          | Y          | Y          | Y            | Y            |
|      | Y        | Y     | Y     | Y     | Y          | Y          | Y          | Y     | Y          | Y          | Y          | Y            | Y            |
|      | C        | C     | C     | C     | C          | C          | C          | C     | C          | C          | C          | C            | C            |
|      | A        | A     | A     | A     | A          | A          | A          | A     | A          | A          | A          | A            | A            |
|      | R        | R     | R     | R     | R          | R          | R          | R     | R          | R          | R          | R            | R            |
|      |          | G     | G     | G     | V          | V          | V          | A     | D          | G          | G          | D            | D            |
|      |          | A     | G     | E     | A          | A          | A          | G     | P          | A          | T          | S            | Q            |
|      |          | R     | H     | R     | P          | P          | P          | L     | R          | V          | M          | Y            | G            |
|      |          | I     | F     | L     | L          | L          | L          | L     | G          | V          | I          | Y            | T            |
| CDR3 |          | I     | G     | G     | G          | G          | G          | G     | A          | V          | V          | D            | G            |

**Figure 2C**

| CDR | DP5<br>0 | 3.1.1 | 4.1.1 | 4.8.1 | 4.10.<br>2 | 4.13.<br>1 | 4.14.<br>3 | 6.1.1 | 11.2.<br>1 | 11.6.<br>1 | 11.7.<br>1 | 12.3.<br>1.1 | 12.9.<br>1.1 |
|-----|----------|-------|-------|-------|------------|------------|------------|-------|------------|------------|------------|--------------|--------------|
|     |          | T     | P     | S     | P          | P          | P          | Y     | T          | P          | V          | F            | W            |
|     |          | P     | F     | Y     | L          | L          | L          | F     | L          | A          | G          | W            | Y            |
|     |          | C     | D     | F     | D          | D          | D          | D     | Y          | A          | T          | S            | G            |
|     |          | M     | Y     | D     | Y          | Y          | Y          | Y     | Y          | M          | L          | G            | G            |
|     |          | D     | W     | Y     | W          | W          | W          | W     | Y          | D          | D          | R            | F            |
|     |          | V     | G     | W     | G          | G          | G          | G     | Y          | V          | Y          | G            | D            |
|     |          | W     | Q     | G     | Q          | Q          | Q          | Q     | Y          | W          | W          | G            | F            |
|     |          | G     | G     | Q     | G          | G          | G          | G     | G          | G          | G          | M            | W            |
|     |          | Q     | T     | G     | T          | T          | T          | T     | M          | Q          | Q          | D            | G            |
|     |          | G     | L     | T     | L          | L          | L          | L     | D          | G          | G          | V            | Q            |
|     |          | T     | V     | L     | V          | V          | V          | V     | V          | T          | T          | W            | G            |
|     |          | T     | T     | V     | T          | T          | T          | T     | W          | T          | L          | G            | T            |
|     |          | V     | V     | T     | V          | V          | V          | V     | G          | V          | V          | Q            | L            |
|     |          | T     | S     | V     | S          | S          | S          | S     | Q          | T          | T          | G            | V            |
|     |          | V     | S     | S     | S          | S          | S          | S     | G          | V          | V          | T            | T            |
|     |          | S     | A     | S     | A          | A          | A          | A     | T          | S          | S          | T            | V            |
|     |          | S     | S     | A     | S          | S          | S          | S     | T          | S          | S          | V            | S            |
|     |          | A     | T     | S     | T          | T          | T          | T     | V          | A          | A          | T            | S            |
|     |          | S     | K     | T     | K          | K          | K          | K     | T          | S          | S          | V            | A            |
|     |          | T     | G     | K     | G          | G          | G          | G     | V          | T          | T          | S            | S            |
|     |          | K     | P     | G     | P          | P          | P          | P     | S          | K          | K          | S            | T            |
|     |          | G     | S     | P     | S          | S          | S          | S     | S          | G          | G          | A            | K            |
|     |          | P     | V     | S     | V          | V          | V          | V     | A          | P          | P          | S            | G            |
|     |          | S     | F     | V     | F          | F          | F          | F     | S          | S          | S          | T            | P            |
|     |          | V     | P     | F     | P          | P          | P          | P     | T          | V          | V          | K            | S            |
|     |          | F     | L     | P     | L          | L          | L          | L     | K          | F          | F          | G            | V            |
|     |          | P     | A     | L     | A          | A          | A          | A     | G          | P          | P          | P            | F            |
|     |          | L     | P     | A     | P          | P          | P          | P     | P          | L          | L          | S            | P            |
|     |          | A     | C     | P     | C          | C          | C          | C     | S          | A          | A          | V            | L            |
|     |          | P     | S     | C     | S          | S          | S          | S     | V          | P          | P          | F            | A            |
|     |          | C     | R     | S     | R          | R          | R          | R     | F          | C          | C          | P            | P            |
|     |          | S     | S     | R     | S          | S          | S          | S     | P          | S          | S          | L            | C            |
|     |          | R     | T     | S     | T          | T          | T          | T     | L          | R          | R          | A            | S            |
|     |          | S     | S     | T     | S          | S          | S          | S     | A          | S          | S          | P            | R            |
|     |          | T     | E     | S     | E          | E          | E          | E     | P          | T          | T          | C            | S            |
|     |          | S     | S     | E     | S          | S          | S          | S     | C          | S          | S          | S            | T            |
|     |          | E     | T     | S     | T          | T          | T          | T     | S          | E          | E          | R            | S            |
|     |          | S     | A     | T     | A          | A          | A          | A     | R          | S          | S          | S            | E            |
|     |          | T     | A     | A     | A          | A          | A          | A     | S          | T          | T          | T            | S            |
|     |          | A     | L     | A     | L          | L          | L          | L     | T          | A          | A          | S            | T            |
|     |          | A     | G     | L     | G          | G          | G          | G     | S          | A          | A          | E            | A            |
|     |          | L     | C     | G     | C          | C          | C          | C     | E          | L          | L          | S            | A            |
|     |          | G     | L     | C     | L          | L          | L          | L     | S          | G          | G          | T            | L            |
|     |          | C     | V     | L     | V          | V          | V          |       | T          | C          | C          | A            | G            |
|     |          | L     | K     | V     | K          | K          | K          |       | A          | L          | L          | A            | C            |
|     |          | V     | D     | K     | D          | D          | D          |       | A          | V          | V          | L            | L            |
|     |          | K     | Y     | D     | Y          | Y          | Y          |       | L          | K          | K          | G            | V            |
|     |          | D     | F     | Y     | F          | F          | F          |       | G          | D          | D          | C            | K            |
|     |          | Y     | P     | F     | P          | P          | P          |       | C          | Y          | Y          | L            | D            |

**Figure 2D**

[illegible]

## Figure 3

### DP-65 or 4-31 gene product

VSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSVTAADTA VYYCAR  
CDR1 CDR2

### 2.1.3 Heavy Chain Protein

SGPGLVKPSQILSLTCTVSGGSISSGGHYWSWIRQHPGKGLEWIGYIYYIGNTYYNPSLKSRVTISVDTSKNQFSLKLSVTAADTA VYYCAR  
CDR1 CDR2  
DSGDYYGIDYWGQGTITVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ  
CDR3

## Figure 4

### A27 Gene Product

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQOYGSSE  
 CDR1 CDR2 CDR3

### 4.1.1 Kappa Chain Protein

QSPGTLSLSPGERATLSCRASQSISSSELAWYQQRPQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQOYGTSPWT  
 CDR1 CDR2 CDR3  
 FGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK

### 4.8.1 Kappa Chain Protein

QSPGTLSLSPGERATLSCRISQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQOYGISPET  
 CDR1 CDR2 CDR3  
 FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

### 4.14.3 Kappa Chain Protein

GTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQOYGRSPET  
 CDR1 CDR2 CDR3  
 FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

### 6.1.1 Kappa Chain Protein

QSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGYSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQOYGISPET  
 CDR1 CDR2 CDR3  
 FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

### 4.10.2 Kappa Chain Protein

SPGTLSLSPGERATLSCRASQSISSSELAWYQQKPGQAPRLLIYRPSRATGIPDSFSGSGGTDFLTISRLEPEDFALYYCQOYGTSPET  
 CDR1 CDR2 CDR3  
 FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

### 4.13.1 Kappa Chain Protein

QSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQOYGRSPET  
 CDR1 CDR2 CDR3  
 FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKGG

## Figure 5

### 012 Gene Product

DIQMTQSPSSLSASVGDRVTITCRASQISISYLNWYQQKPGKAPKLLIYAASSLSQGVPSRFRSGSGTDFLTISLQPEDFATYYCQQQSYSTPEI  
 CDR1 CDR2 CDR3

### 3.1.1 Kappa Chain Protein

QSPSSLSASVGDRVTITCRASQISNTYLIWYQQKPGKAPNFIISATSILOSGVPSRFRSGSGTNFTLTINSLHPEDFATYYCQQQSYSTPEI  
 CDR1 CDR2 CDR3  
 FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG

### 11.2.1 Kappa Chain Protein

PSSLSASVGDRVTITCRASQISNSYLDWYQQKPGKAPKLLIYAASSLSQGVPSRFRSGSGTDFLTISLQPEDFATYYCQQQSYSTPEI  
 CDR1 CDR2 CDR3  
 FGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV

### 11.6.1 Kappa Chain Protein

TQSPSSLSASVGDRVTITCRASQISRYLNWYQQKPGKAPKFLIYVASILOSGVPSGFSASGSGPDFLTISLQPEDFATYYCQQQSYSTPEI  
 CDR1 CDR2 CDR3  
 FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN

### 11.7.1 Kappa Chain Protein

TQSPSSLSASVGDRVTITCRASQISNYLNWYQQKPGKAPRVLIYAASSLSQGVPSRFRSGSGIDCTLTISLQPEDFATYYCQQQSYITPEI  
 CDR1 CDR2 CDR3  
 FGPGTRVDIERTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAY

## Figure 6

### A10/A26 Gene Product

EIVLTQSPDFQSVTPKEKVTITCRASQSIGSSLLHWYQQKPDQSPKLLIKYASQSESGVPSRFSGSGGTDFTLTNSLEAEDAATYYCHQSSSLPQ  
CDR1 CDR2 CDR3

### 2.1.3 Kappa Chain Protein

SPDFQSVTPKEKVTITCRASQSIGSSLLHWYQQKPDQSPKLLIKYASQSESGVPSRFSGSGGTDFTLTNSLEAEDAATYYCHQSSSLPLT  
CDR1 CDR2 CDR3  
FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE



## Figure 7

### A17 Gene Product

DVVMTQSPVTLGQPASISCRSSQSLYYSDGNITVLLNWFOQRPQGSPRRLLYKVSNRDSGVPDFRSGSGGTDFTLKISRVEAEDVGVYYCMQGHWP  
CDR1 CDR2 CDR3

### 12.3.1 Kappa Chain Protein

PLSLPVTLGQPASISCRSSQSLYYSDGNITVLLNWFOQRPQGSPRRLLYKVSNWDSGVPDFRSGSGGTDFTLKISRVEAEDVGVYYCMQGSHPPT  
CDR1 CDR2 CDR3  
FGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP

## Figure 8

### A3/A19 Gene Product

DIVMTQSP<sup>1</sup>LSLPVTPGEPASISCRSSQSL<sup>2</sup>LHSNGYN<sup>3</sup>YLDWYLQKPGQSPQLLIYLG<sup>4</sup>SNRASGV<sup>5</sup>PDFRFSGSGGTDF<sup>6</sup>TLKISRVEAEDVG<sup>7</sup>VYYCMQALQ<sup>8</sup>ITP  
CDR1 CDR2 CDR3

### 2.9.1 Kappa Chain Protein

PGEPASISCRSSQSL<sup>2</sup>LHSNGYN<sup>3</sup>YLDWYLQKPGQSPQLLIYLG<sup>4</sup>SNRASGV<sup>5</sup>PDFRFSGSGGTDF<sup>6</sup>TLKISRVEAEDVG<sup>7</sup>VYYCMQALQ<sup>8</sup>ITLT  
CDR1 CDR2 CDR3  
FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC<sup>9</sup>LLNNFYPR

**Figure 9** Amino-terminal amino acid sequence analysis

| Hybridoma | Light chain  | MW     |
|-----------|--|--------|
| CT2.1.3   | ND   | ND     |
| CT3.1.1   | NH <sub>2</sub> -DIQMTQSPSSLSASVGDRV   | 26,119 |
| CT4.1.1   | NH <sub>2</sub> -EIVLTQSPGTLSPGERAT  | 23,917 |
| CT4.8.1   | NH <sub>2</sub> -EIVLTQSPGTLSPGERAT  | 23,617 |
| CT4.9.1   | NH <sub>2</sub> -DIQMTQSPSSVSASVGDRV   | 23,702 |
| CT4.10.2  | NH <sub>2</sub> -TGEFVLTQSPGTLSPGER (60%)<br>NH <sub>2</sub> -EFVLTQSPGTLSPGERAT (40%) | 24,101 |
| CT4.14.3  | NH <sub>2</sub> -EIVLTQSPGTLSPGERAT  | 23,770 |
| CT4.13.1  | NH <sub>2</sub> -EIVLTQSPGTLSPGERAT  | 23,802 |
| CT6.1.1   | NH <sub>2</sub> -EIVLTQSPGTLSPGERAT  | 23,747 |

| Hybridoma | Heavy chain  | MW     |
|-----------|--|--------|
| CT2.1.3   | ND   | ND     |
| CT3.1.1   | NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase:<br>NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~80%)<br>NH <sub>2</sub> -PEVQF...(minor sequence~20%)           | 51,813 |
| CT4.1.1   | NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase:<br>NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~65%)<br>NH <sub>2</sub> -PEVQFNWYVD...(minor sequence~35%)      | 51,502 |
| CT4.8.1   | NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase:<br>NH <sub>2</sub> -pQ-VQLVESGGGVVQPG(R)SL... (major sequence~60%)<br>NH <sub>2</sub> -PEVQFNWY...(minor sequence~40%)      | 51,597 |
| CT4.9.1   | NH <sub>2</sub> -EVQLLES GGGLVQPGSLRL (free amino terminus)  | 51,437 |
| CT4.10.2  | NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase:<br>NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~60%)<br>NH <sub>2</sub> -PEVQFNWYVD...(minor sequence~40%)      | 51,502 |
| CT4.14.3  | NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase:<br>NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSL(R)(L)(S) (major sequence~65%)<br>NH <sub>2</sub> -PEVQFNWYV...(minor sequence~35%) | 51,293 |
| CT4.13.1  | NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase:<br>NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~75%)<br>NH <sub>2</sub> -PEVQFN...(minor sequence~25%)          | 51,305 |
| CT6.1.1   | NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase:<br>NH <sub>2</sub> -pQ-VQLVESGGGVVEPGRSLRLS* (major sequence~65%)<br>NH <sub>2</sub> -PEVQFNWYVD... (minor sequence~35%)    | 51,476 |

\* This heavy chain sequence is similar to the other blocked heavy chain sequences except for a unique Gln->Glu change at position 13.

Figure 10A

| antibody  | Conc. (mg/ml) (Ec1.58) |          | IEF     | SDS-PAGE    |          | SEC     | reported MALDI |        | n-term. seq. (lc)*        |                           |
|---|------------------------|----------|---------|-------------|----------|---------|----------------|--------|---------------------------|---------------------------|
|   | reported               | observed |         | (+) b-me    | (-) b-me |         | Hc             | Lc     | reported                  | observed                  |
| CT 3.1.1  | 1.1                    | 1.57     | smear   | 50 & 28 kDa | 6 bands  | 139,400 | 51,813         | 26,119 | DIQMTQSP (SEQ ID NO: 141) | DIQMTQSP (SEQ ID NO: 141) |
| CT 4.1.1  | 1.54                   | 1.65     | smear   | 50 & 24 kDa | 6 bands  | 79,900  | 51,502         | 23,917 | EIVLTQSP (SEQ ID NO: 142) | EIVLTQSP (SEQ ID NO: 142) |
| CT 4.8.1  | 1.52                   | 1.54     | 4 bands | 50 & 24 kDa | 6 bands  | 110,300 | 51,597         | 23,617 | EIVLTQSP (SEQ ID NO: 143) | EIVLTQSP (SEQ ID NO: 143) |
| CT 4.10.2   | 1.29                   | 1.77     | 4 bands | 50 & 25 kDa | 6 bands  | 107,200 | 51,502         | 24,101 | **                        | ***                       |
| CT 4.14.3   | 1.75                   | 1.65     | smear   | 50 & 24 kDa | 6 bands  | 82,800  | 51,293         | 23,770 | EIVLTQSP (SEQ ID NO: 146) | EIVLTQSP (SEQ ID NO: 146) |
| CT 6.1.1  | 1.36                   | 1.3      | 4 bands | 50 & 24 kDa | 6 bands  | 101,100 | 51,476         | 23,747 | EIVLTQSP (SEQ ID NO: 147) | EIVLTQSP (SEQ ID NO: 147) |
| * all heavy chains n-terminally blocked (not sequenced in-house)                              |                        |          |         |             |          |         |                |        |                           |                           |
| ** mixed sequence reported: TGEFVLTQSP (60) (SEQ ID NO: 144) & EFVLTQSP (40) (SEQ ID NO: 145) |                        |          |         |             |          |         |                |        |                           |                           |
| *** mixed sequence observed TGEFVLTQSP (60) (SEQ ID NO: 144) & EFVLTQSP (40) (SEQ ID NO: 145) |                        |          |         |             |          |         |                |        |                           |                           |

$\text{IOD}_{280\text{nm}} = 0.633 \text{ mg/ml}$   
 Ec-1.58

Figure 10B

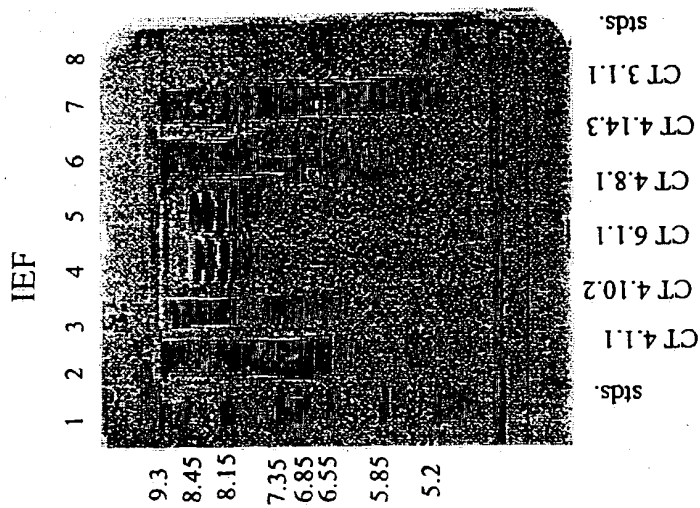


Figure 10C

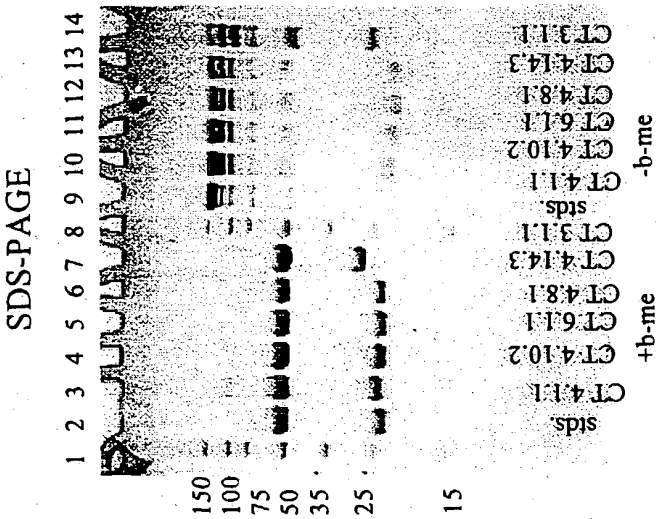
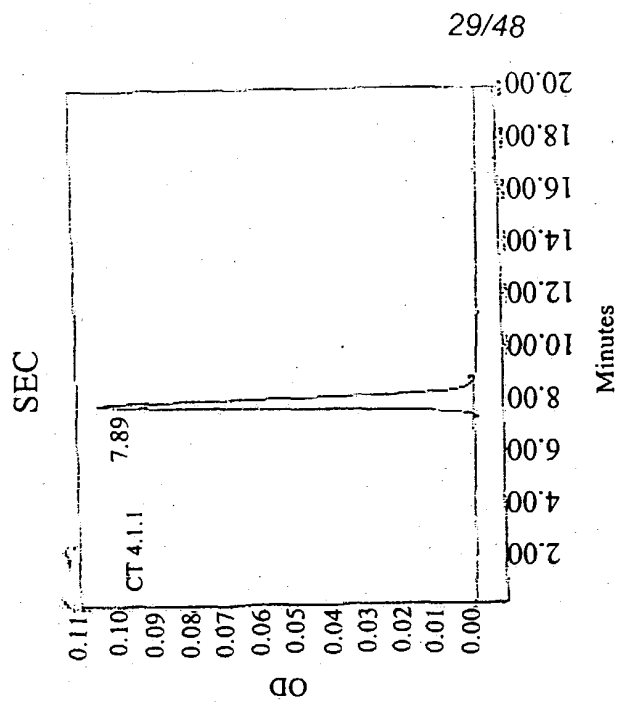
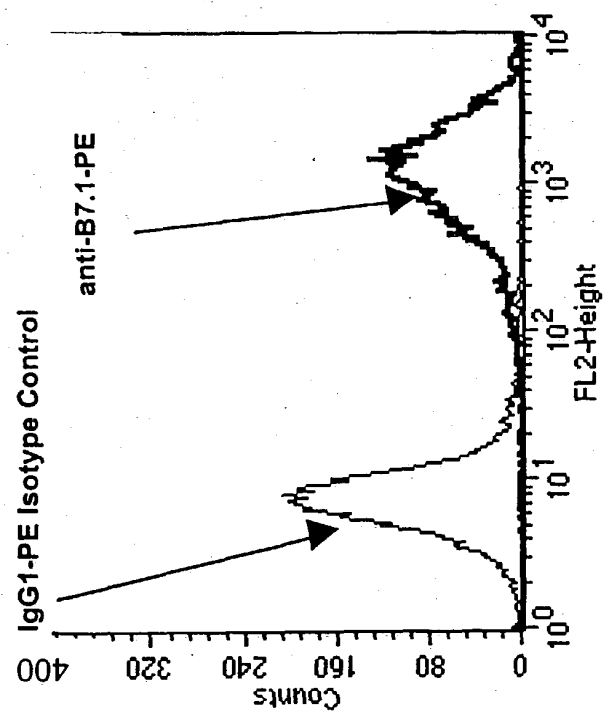


Figure 10D



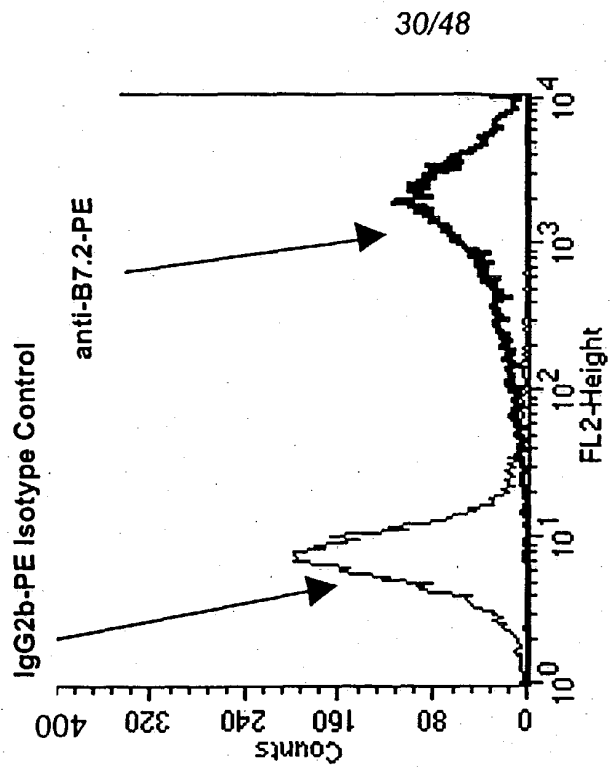
**Figure 11A**



99.7% B7.1 pos.

Expression of B7.1 and B7.2 on Raji Cells

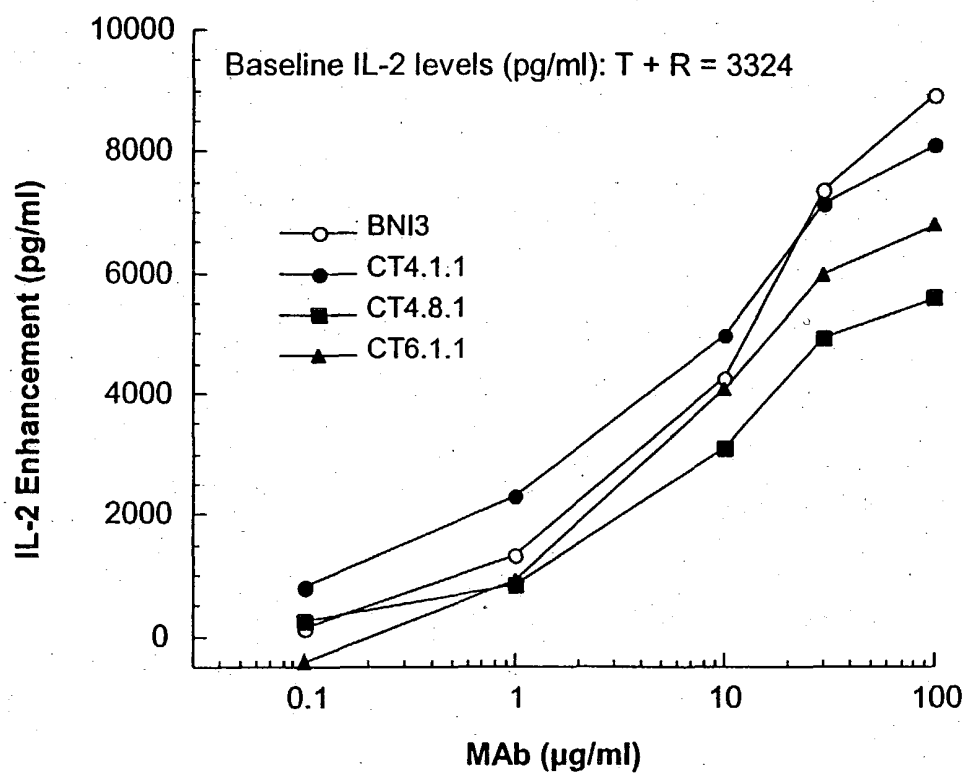
**Figure 11B**



99.7% B7.2 pos.

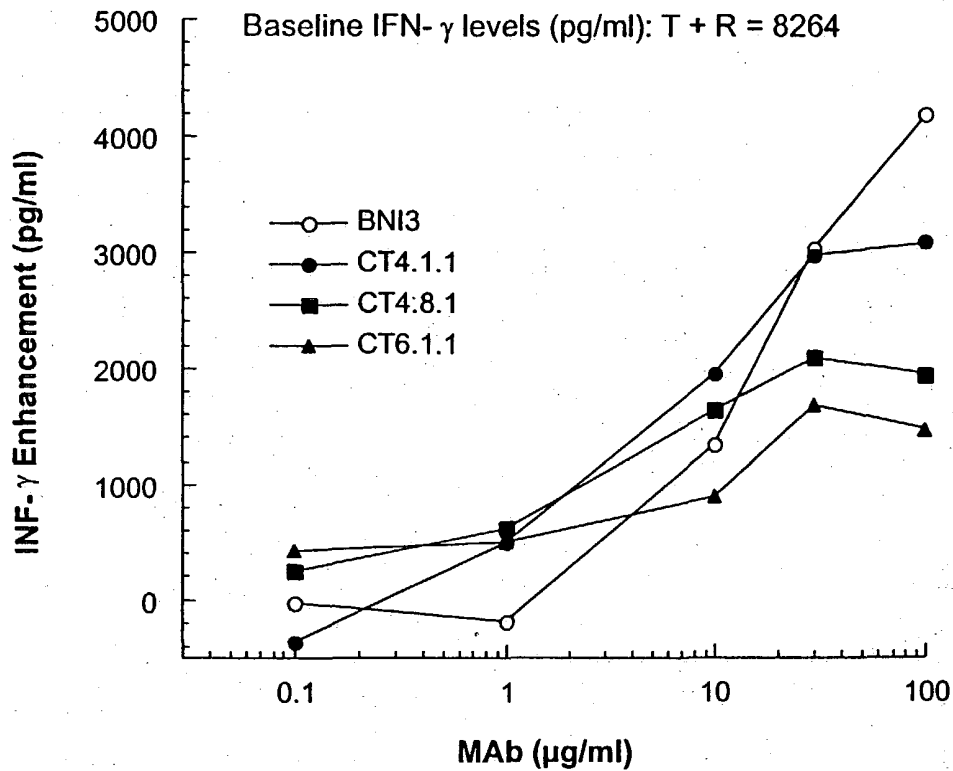
**Figure 12**

**Enhancement of Human T Cell IL-2 Production  
Induced by Anti-CTLA4 XenoMouse MAbs in  
the 72 Hour T Blast / Raji Assay**



**Figure 13**

**Enhancement of Human T Cell IFN- $\gamma$  Production  
Induced by Anti-CTLA4 XenoMouse MAbs in  
the 72 Hour T Blast / Raji Assay**

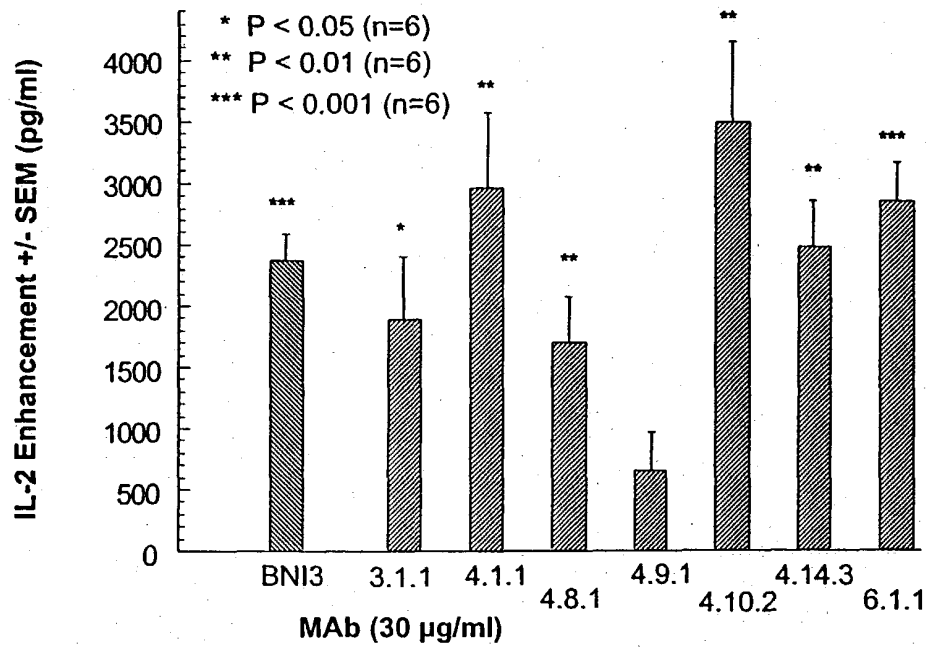




## Figure 14

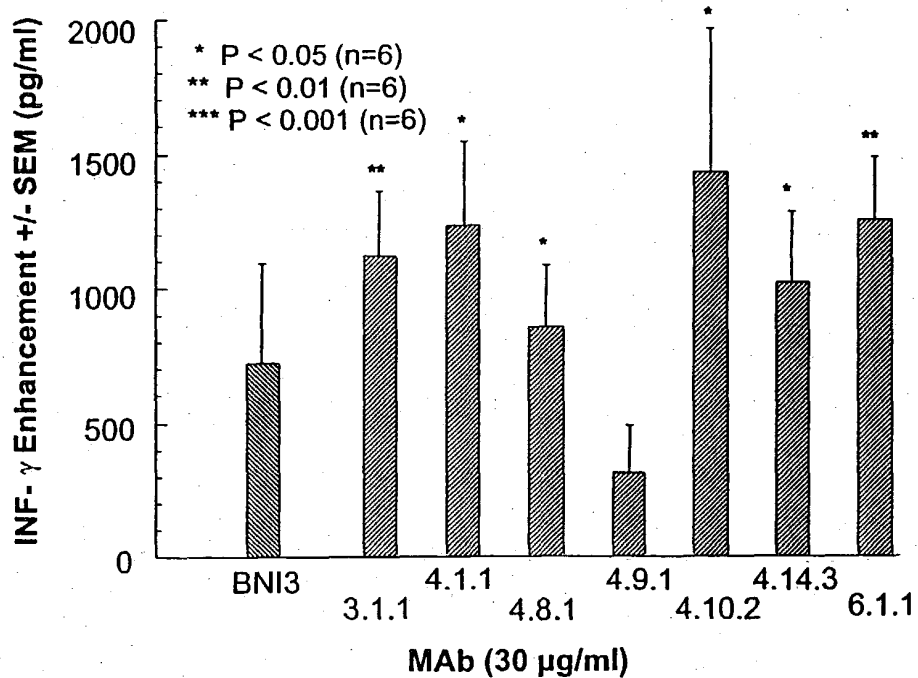
### Enhancement of Human T Cell IL-2 Production Induced by Anti-CTLA4 XenoMouse MABs in the 72 Hour T Blast / Raji Assay (6 Donors)

Baseline IL-2 levels (pg/ml): T + R = 9187, T + R + IgG2a = 9389, T + R + IgG2 = 8509



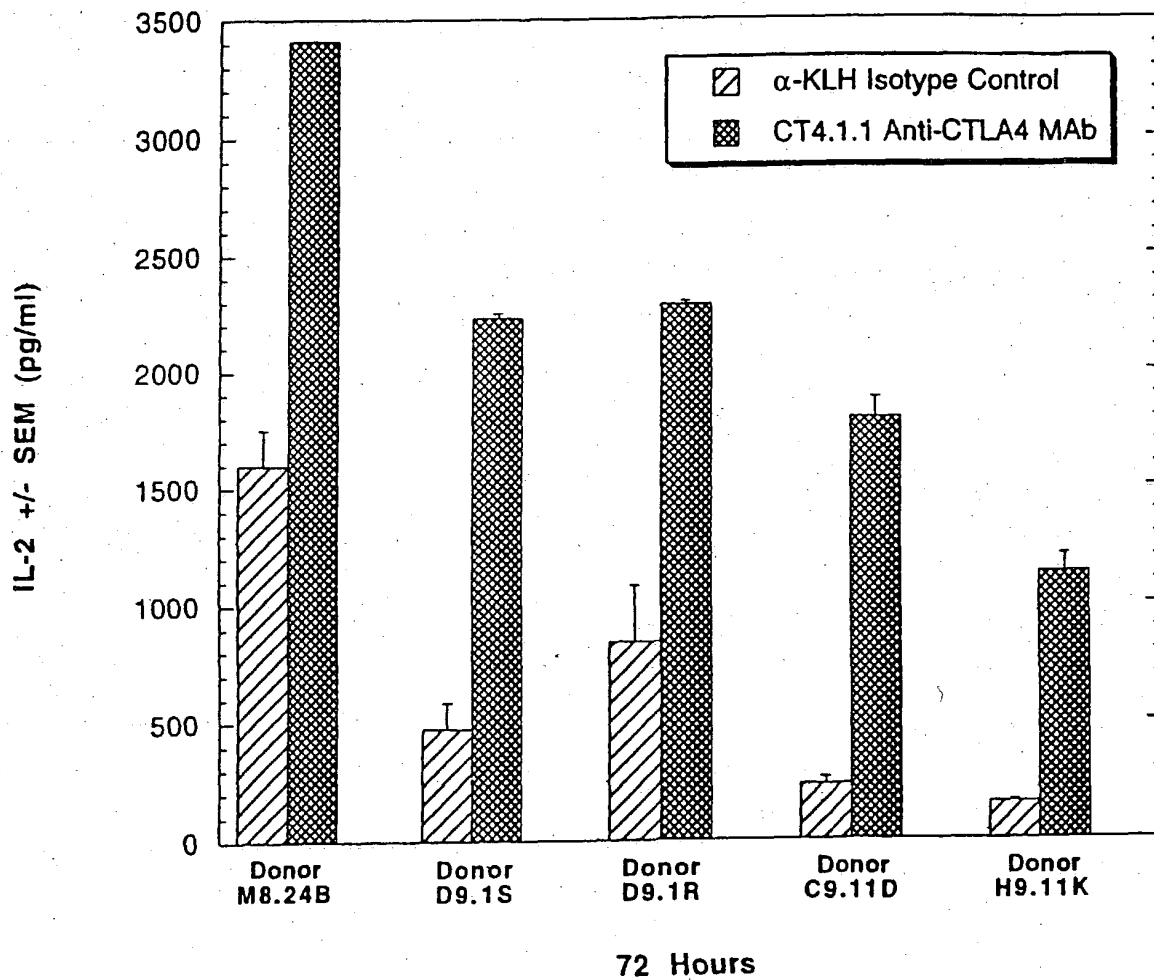
**Figure 15**

**Enhancement of Human T Cell IFN- $\gamma$  Production  
Induced by Anti-CTLA4 XenoMouse MAbs in  
the 72 Hour T Blast / Raji Assay (6 Donors)**  
Baseline IFN- $\gamma$  levels (pg/ml): T + R = 4780, T + R + IgG2a = 4868, T + R + IgG2 = 4331



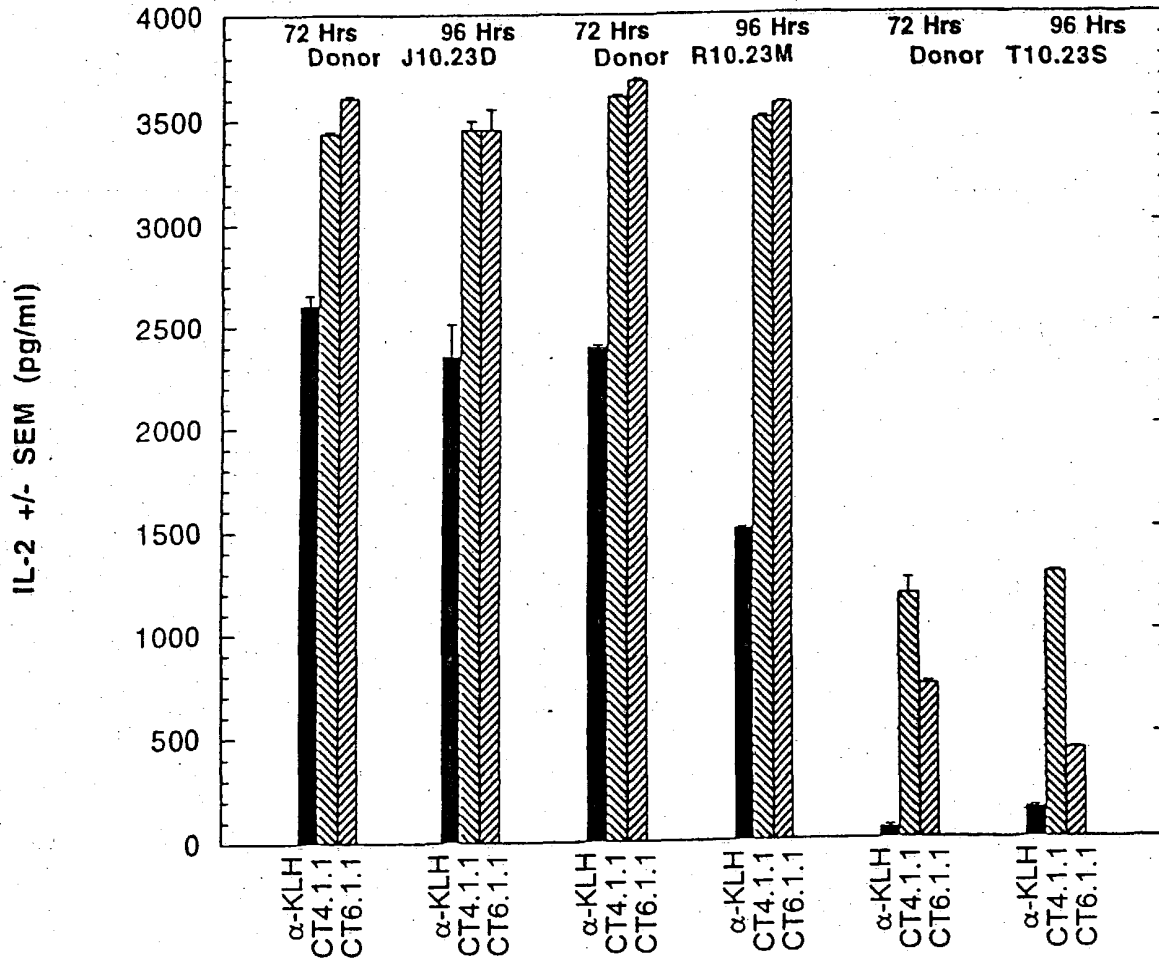
**Figure 16**

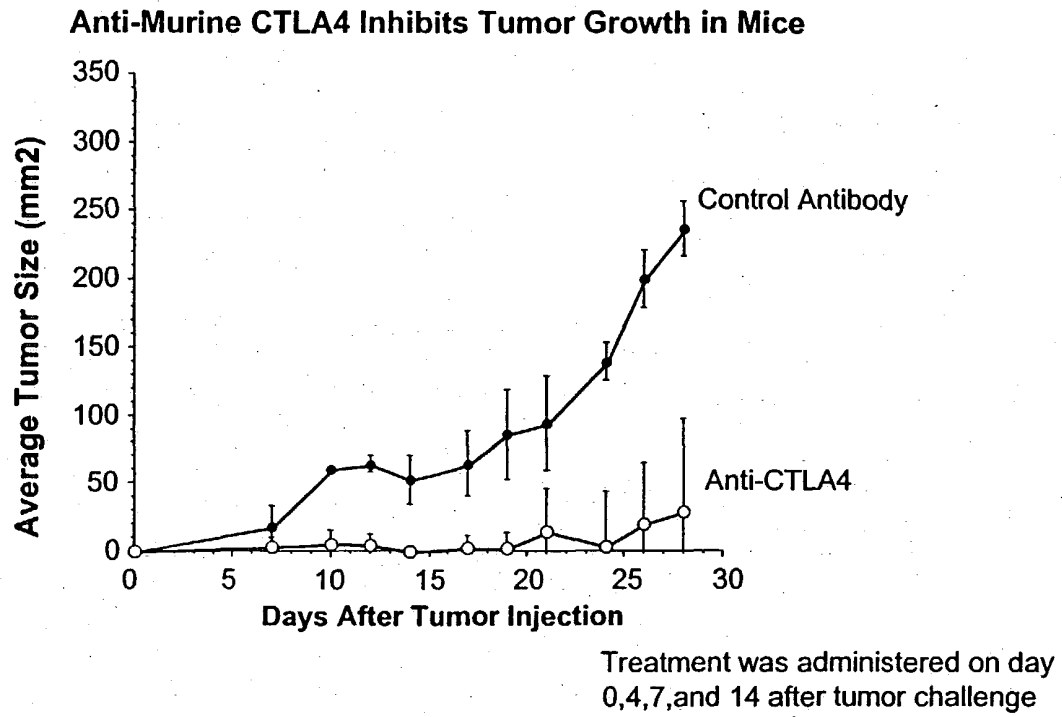
**Enhancement of IL-2 Production Induced by Anti-CTLA4 MAb CT4.1.1 (30  $\mu$ g/ml) Binding to Human PBMC Stimulated with SEA (100 ng/ml) Plus Anti-CD3 MAb (60 ng/ml)**



**Figure 17**

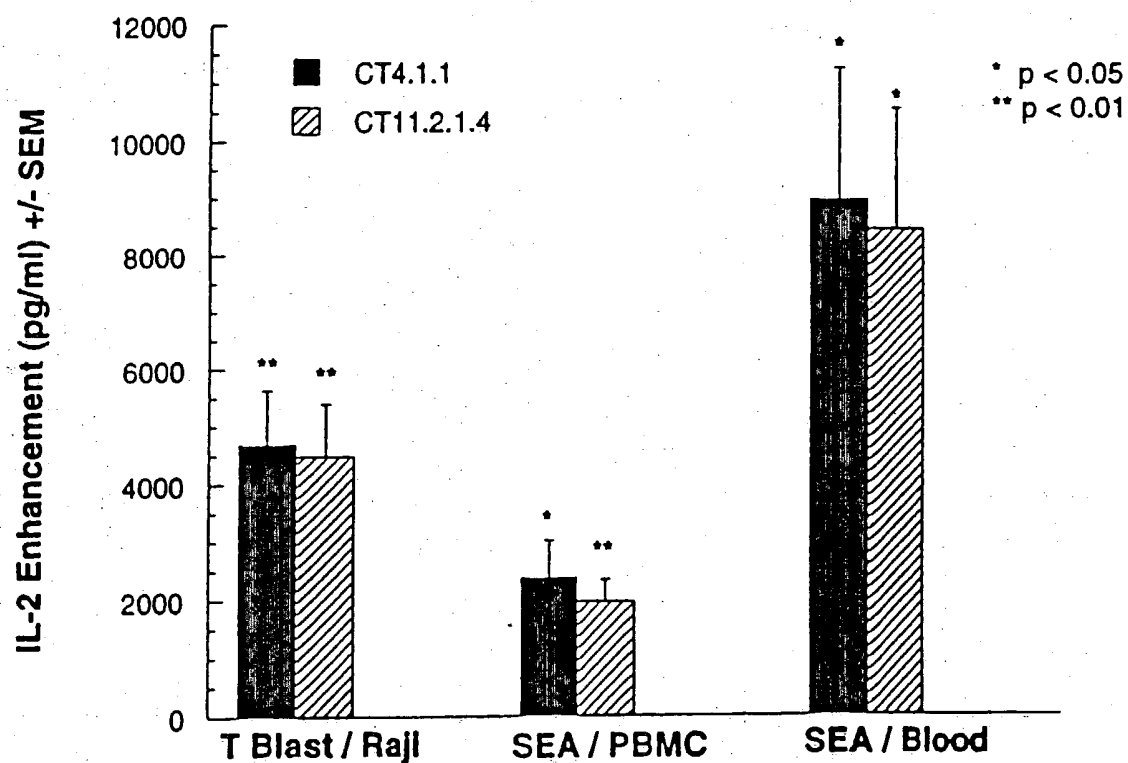
Enhancement of IL-2 Production Induced by Anti-CTLA4 MAbs  
(30  $\mu$ g/ml) in Human Whole Blood Stimulated with SEA  
(100 ng/ml) Plus Anti-CD3 MAb (60 ng/ml)



**Figure 18**

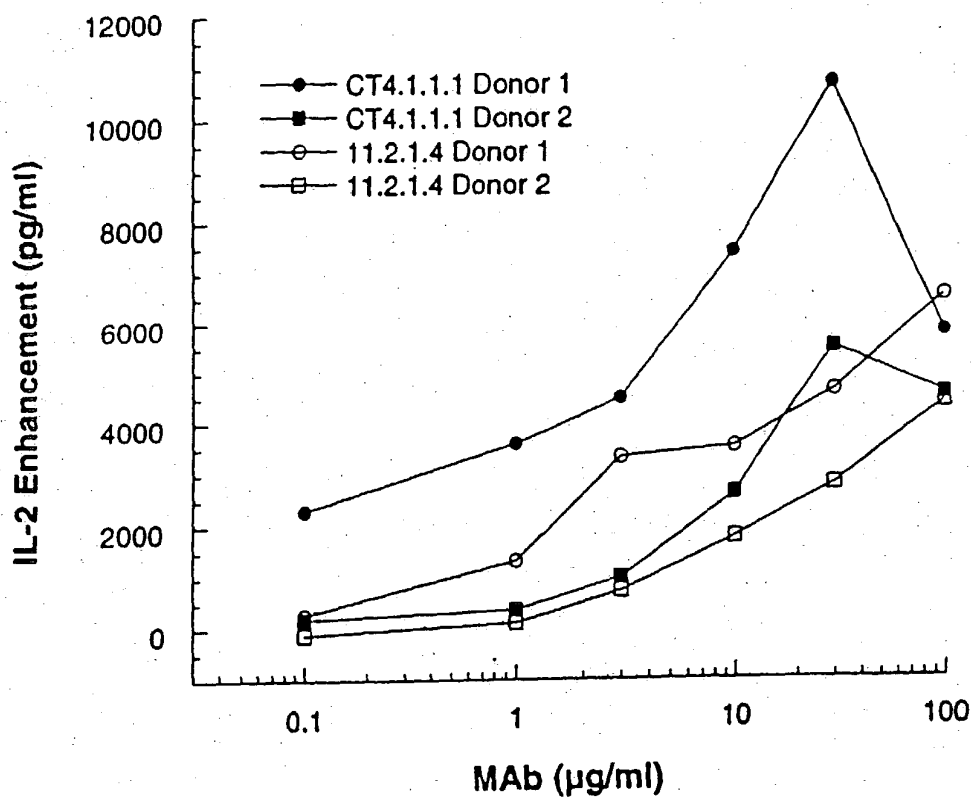
**Figure 19**

**Enhancement of IL-2 Production Induced by Anti-CTLA4 MAbs  
(30  $\mu$ g/ml) in the 72 Hour T Blast / Raji and  
Superantigen Assays (6 Donors)**



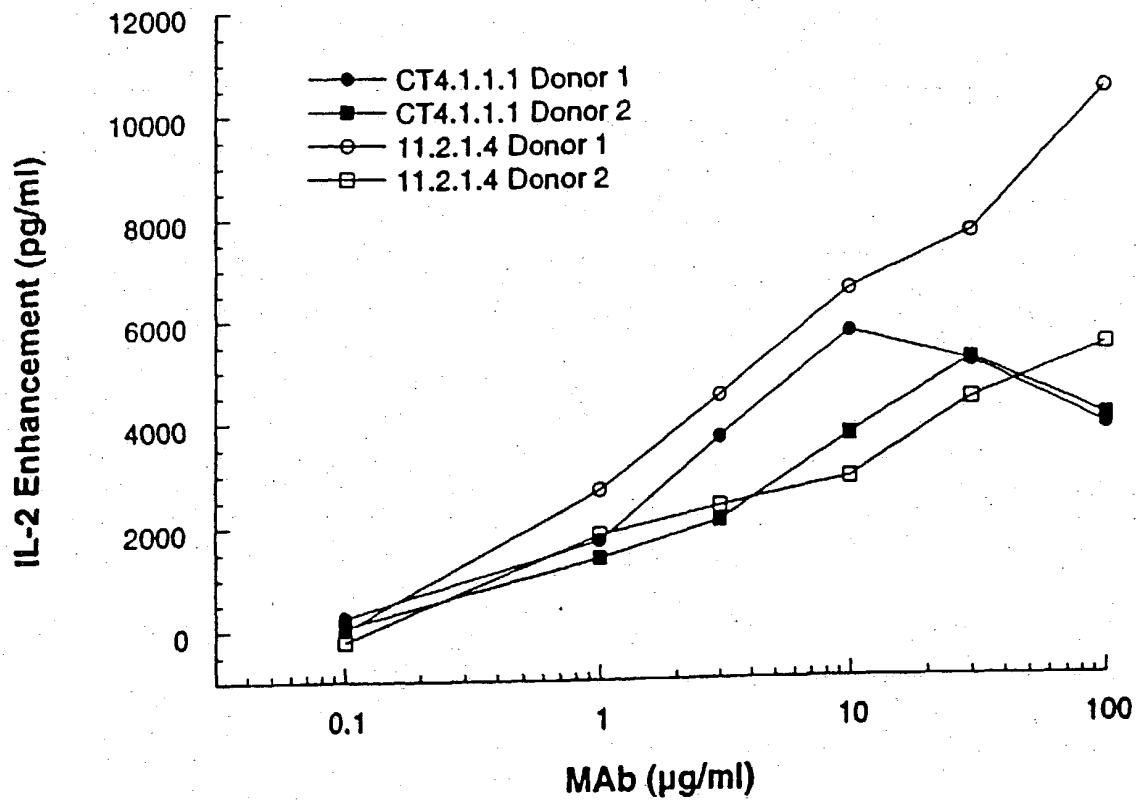
**Figure 20**

**Enhancement of Human T Cell IL-2 Production  
Induced by Anti-CTLA4 MAbs in  
the 72 Hour T Blast / Raji Assay**



**Figure 21**

**Enhancement of IL-2 Production Induced by Anti-CTLA4  
MAbs in Whole Blood Stimulated with  
Superantigen (100 ng/ml)**





- Signal peptides shown in bold and large text
- Open reading frame for genomic clone underlined
- Mutations introduced to make deglycosylated Ab (N294Q) double underlined and large text

**Figure 22A** 4.1.1 IgG2 Heavy Chain cDNA

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTACCTTCAGTAG  
 CCATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGAAATAAATACTATGCAGACTCCGTGAAGGGC  
 CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTCACT  
 TCGGTCCTTTTGACTACTGGGGCCAGGGAACCCTGGTCAACGCTCTCCTCAGCC  
 TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC  
 CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG  
 TGACGGTGTTCGTGGAACCTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCA  
 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC  
 CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTCAGATCACAAGCCCA  
 GCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTTCGAGTGCCCA  
 CCGTGCCCAGCACCACTGTGGCAGGACCGTCAGTCTTCCCTCTTCCCCCCTAAA  
 ACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGG  
 TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC  
 GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCAC  
 GTTCCGTGTGGTCAGCGTCCTCACCCTTGTGCACCAGGACTGGCTGAACGGCA  
 AGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCAGCCCCCATCGAGAAA  
 ACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC  
 CCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCA  
 AAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG  
 GAGAACAATAACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTT  
 CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT  
 TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC  
 CTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:53)

**Figure 22B** 4.1.1 IgG2 Heavy Chain Genomic DNA

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTACCTTCAGTAG  
 CCATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGAAATAAATACTATGCAGACTCCGTGAAGGGC  
 CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTCACT  
 TCGGTCTTTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCCTCAGCT  
 AGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC  
 CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG  
 TGACGGTGTGCTGGAACCTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCA  
 GCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC  
 CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCA  
 GCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGG  
 GTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTG  
 CAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCCATCTGTCTCCTCACCCGAGG  
 CCTCTGCCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC  
 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCTACCCAGGCCCTTCACACACA  
 GGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGC  
 CCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGAC  
 ACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGAGCGC  
 AAATGTTGTGTCGAGTGCCCAACCGTGCCCAAGGTAAGCCAGCCAGGCCTCGCC  
 CTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGG  
 CCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCCTCAGCACCACCTGT  
 GGCAGGACCGTCAGTCTTCCCTCTTCCCCCAAAACCCAAGGACACCCTCATGA  
 TCTCCCGGACCCCTGAGGTACGTGCGTGGTGGTGGACGTGAGCCACGAAGAC  
 CCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAA  
 GACAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCC  
 TCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTC  
 TCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGG  
 TGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCACCC  
 TCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCG  
 AGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACC  
 AGGTACGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCGTG  
 GAGTGGGAGAGCAATGGGCAGCCGGAACAACACTACAAGACCACACCTCCCAT  
 GCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGA  
 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTG  
 CACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ  
 ID NO:54)

**Figure 22C** 4.1.1 IgG2 Heavy Chain Protein

**MEFGLSWVFLVALLRGVQC**QVQLVESGGGVVQPGRSLRLSCVASGFTFSS  
 HGMHWVRQAPGKLEWVAVIWDGRNKYYADSVKGRFTISRDN SKNTLFLQMN  
 SLRAEDTAVYYCARGGHFGPFDYWGGTLTVTVSSASTKGPSVFPLAPCSRSTS  
 ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP  
 SSNFGTQTYTCNV DHKPSNTKVDKTV ERKCCVECP PCPAPPVAGPSVFLFPPK  
 PKDTLMI SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST  
 FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL P  
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSFF  
 LYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK (SEQ ID  
 NO:63)

**Figure 22D** 4.1.1 IgG2 Heavy Chain cDNA N294Q

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTACCTTCAGTAG  
 CCATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGAAATAAATACTATGCAGACTCCGTGAAGGGC  
 CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTCACT  
 TCGGTCTTTTACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAGCC  
 TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC  
 CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG  
 TGACGGTGTTCGTGGAACCTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCA  
 GCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC  
 CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCCA  
 GCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTCGAGTGCCCCA  
 CCGTGCCCAGCACCACTGTGGCAGGACCGTCAGTCTTCTCTTCCCCCCTAA  
 ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGG  
 TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC  
 GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTT**CCA**AAGCAC  
 GTTCCGTGTGGTCAGCGTCTCACCCTGTGTCACCAGGACTGGCTGAACGGCA  
 AGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAA  
 ACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCC  
 CCCATCCCGGGAGGAGATGACCAAGAACCAGGTGACCTGCCTGGTCA  
 AAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG  
 GAGAACAACCTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTT  
 CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT  
 TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC  
 CTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:55)

**Figure 22E** 4.1.1 IgG2 Heavy Chain Protein N294Q

**MEFGLSWVFLVALLRGVQC**QVQLVESGGGVVQPGRSLRLSCVASGFTFSS  
 HGMHWVRQAPGKLEWVAVIWDGRNKYYADSVKGRFTISRDNKNTLFLQMN  
 SLRAEDTAVYYCARGGHFGPFDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTS  
 ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP  
 SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPK  
 PKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQ**Q**ST  
 FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL  
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSGSGFF  
 LYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK (SEQ ID  
 NO:64)

**Figure 22F** 4.1.1 Kappa Chain DNA

**ATGGAAACCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTC**  
**CCAGATAACCACCGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC**  
 TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTATTA  
 GCAGCAGCTTCTTAGCCTGGTACCAGCAGAGACCTGGCCAGGCTCCCAGGCTC  
 CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAAGTGG  
 CAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAG  
 ATTTTGCAGTGTATTACTGTCAGCAGTATGGTACCTCACCTGGACGTTCCGGC  
 CAAGGGACCAAGGTGGAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT  
 CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCC  
 TGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAAC  
 GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA  
 CAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGA  
 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCCGT  
 ACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:56)

**Figure 22G** 4.1.1 Kappa Chain Protein

**METPAQLLFLLLLWLDPDTTGE**IVLTQSPGTLSPGERATLSCRASQSSIS  
 SSFLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED  
 FAVYYCQOYGTSPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL  
 LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADYEK  
 HKVYACEVTHQGLSSPVTKSFNREGC (SEQ ID NO:65)

**Figure 22H** 4.8.1 Heavy Chain DNA

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTACAGCGTCTGGATTACCTTCAGTAA  
 CTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGTAATAAACACTATGGAGACTCCGTGAAGGGC  
 CGATTACCATCTCCAGTGACAATTCCAAGAACACGCTGTATCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGAGAGAC  
 TGGGGTCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA  
 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCAC  
 CTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAAC  
 CGGTGACGGTGTCTGTGGAAGTCAAGGCGCTCTGACCAGCGGCGTGCACACCTTC  
 CCAGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGT  
 GCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGC  
 CCAGCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTCGAGTGC  
 CCACCGTGCCAGCACCACTGTGGCAGGACCGTCAGTCTTCTTCCCCCCC  
 AAAACCCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGG  
 TGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGAC  
 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAG  
 CACGTTCCGTGTGGTCAGCGTCTCACCCTGTGTCACCAGGACTGGCTGAACG  
 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAG  
 AAAACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT  
 GCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGG  
 TCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG  
 CCGGAGAACAACACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTT  
 CTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACG  
 TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG  
 AGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:57)

**Figure 22I** 4.8.1 Heavy Chain Protein

MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGRSLRLSCTASGFTFSN  
 YGMHWVRQAPGKGLEWVAVIWDGNSKHYGDSVKGRFTISSDNSKNTLYLQMN  
 SLRAEDTAVYYCARGERLGSYFDYWGQGLTVTVSSASTKGPSVFPLAPCSRST  
 SESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV  
 PSSNFGTQTYTCNVDPKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPP  
 KPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS  
 TFRVSVSLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL  
 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSDGSF  
 FLYSKLTVDKSRWQQGNVFSVSMHEALHNHYTQKSLSLSPGK (SEQ ID  
 NO:66)

**Figure 22J** 4.8.1 Kappa Chain DNA

ATGGAAACCCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTC  
 CCAGATAACCACCGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC  
 TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGACCAGTGTTAGCAGCA  
 GTTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC  
 TATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAAGTGGCAGTGG  
 GTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTG  
 CAGTCTATTACTGTGAGCAGTATGGCATCTCACCTTCACTTTTCGGCGGAGGG  
 ACCAAGGTGGAGATCAAGCGAAGTGTGGCTGCACCATCTGTCTTCATCTTCCC  
 GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGCTGCTGA  
 ATAACCTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTC  
 CAATCGGGTAAGTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCAC  
 CTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACA  
 AAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG  
 AGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:58)

**Figure 22K** 4.8.1 Kappa Chain Protein

METPAQLLFLLLLWLPDTTGEIVLTQSPGTLSSLSPGERATLSRSTSVSSS  
 YLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA  
 VYYCQQYGISPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLN  
 NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHK  
 VYACEVTHQGLSPVTKSFNRGEC (SEQ ID NO:67)

**Figure 22L** 6.1.1 Heavy Chain DNA

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCGAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTACAGCGTCTGGATTACCTTCAGTAG  
 TTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGCAATAAACTATGCAGACTCCGCGAAGGGC  
 CGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGACTGC  
 TGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC  
 TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC  
 CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG  
 TGACGGTGTCTGTGGAACCTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCA  
 GCTGTCTTACAGTCTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC  
 CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCA  
 GCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTCGAGTGCCCA  
 CCGTGCCAGCACCACTGTGGCAGGACCGTCAGTCTTCTTCCCCCCCCAAA  
 ACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACGTGCGTGGTGG  
 TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC  
 GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCAC  
 GTTCCGTGTGGTTCAGCGTCTCTCACCGTTGTGCACCAGGACTGGCTGAACGGCA  
 AGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAA  
 ACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC  
 CCCATCCCCGGGAGGAGATGACCAAGAACCAGGTTCAGCCTGACCTGCCTGGTCA  
 AAGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG  
 GAGAACAATAACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTT  
 CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT  
 TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC  
 CTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:59)

**Figure 22M** 6.1.1 Heavy Chain Protein

**MEFGLSWVFLVALLRGVQC**QVQLVESGGGVVEPGRSLRLSCTASGFTFSS  
 YGMHWVRQAPGKGLEWVAVIWDGSENKHYADSAKGRFTISRDNKNTLYLQMN  
 SLRAEDTAVYYCARAGLLGYFDYWGQGLVTVSSASTKGPSVFPLAPCSRSTS  
 ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP  
 SSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPCPAPPVAGPSVFLFPPK  
 PKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST  
 FRVVSIVLTIVHVDWLNQKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLF  
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSFF  
 LYSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID  
 NO:68)

**Figure 22N** 6.1.1 Kappa Chain DNA

**ATGGAAACCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTC**  
**CCAGATAACCACCGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC**  
 TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGTAGGGCCAGTCAAAGTGTTA  
 GCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCCCTC  
 ATCTATGGTGTATCCAGCAGGGCCACTGGCATCCCAGACAGGTTTCAAGTGGCAG  
 TGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATT  
 TTGCAGTGTATTACTGTGTCAGCAGTATGGTATCTCACCATTCACTTTCGGCCCT  
 GGGACCAAAGTGGATATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTT  
 CCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGC  
 TGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCC  
 CTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAG  
 CACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAAC  
 ACAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACA  
 AAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:60)

**Figure 22O** 6.1.1 Kappa Chain Protein

**METPAQLLFLLLLWLPDTTGEIVLTQSPGTLSSLSPGERATLSCRASQSVS**  
 SYLAWYQQKPGQAPRPLIYGVSRRATGIPDRFSGSGSGTDFTLTISRLEPEDF  
 AVYYCQQYGISPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL  
 NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADYEKH  
 KVIYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:69)

**Figure 22P** 11.2.1 IgG2 Heavy Chain DNA:

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAG  
 CTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC  
 CGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCGAGGG  
 GAGCTACCCTTTACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACC  
 ACGGTACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC  
 GCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCA  
 AGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGGCGCTCTGACC  
 AGCGGCGTGCACACCTTCCCAGCTGTCTTACAGTCCTCAGGACTCTACTCCCT  
 CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCT  
 GCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGC  
 AAATGTTGTGTGAGTGCCACCGTGCCAGCACCACCTGTGGCAGGACCGCTC  
 AGTCTTCTCTTCCCCCAAAACCCAGGACACCCCTCATGATCTCCCCGACCC  
 CTGAGGTACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCGAGGTCCAG  
 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACG  
 GGAGGAGCAGTTCAACAGCACGTTCGGTGTGGTCAAGCTCCTCACCCTGTGTG  
 ACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGGC  
 CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAGGGCAGCCCCGAGA  
 ACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGG  
 TCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG  
 TGGGAGCAATGGGCAGCCGGAGAACAATAAGACCAACACCTCCCCTGAGTCT  
 GGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAAGAGCA  
 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC  
 AACCCTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID  
 NO:61)

**Figure 22Q** 11.2.1 IgG2 Heavy Chain Protein:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWY  
 DGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDPRGATLY  
 YYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFP  
 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDH  
 KPSNTKVDKTKVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTC  
 VVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHQDWL  
 NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTC  
 LVKGFYPSDIAVEWESNGQPENNYKTPPMLDSGSSFFLYSKLTVDKSRWQQG  
 NVFSCSVMHREALHNHYTQKSLSLSPGK (SEQ ID NO:70)

**Figure 22R** 11.2.1 IgG2 Kappa Chain DNA:

ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTACTC  
 TGGCTCCGAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCCT  
 CCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAG  
 AGCATTAACAGCTATTTAGATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA  
 ACTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA  
 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT  
 GAAGATTTTGCAACTTACTACTGTCAACAGTATTACAGTACTCCATTCACTTT  
 CGGCCCTGGGACCAAAGTGGAATCAAACGAACTGTGGCTGCACCATCTGTCT  
 TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTG  
 TGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGA  
 TAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCA  
 AGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTAC  
 GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC  
 CGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGTGA (SEQ ID NO:62)

**Figure 22S** 11.2.1 IgG2 Kappa Chain Protein:

DIQMTQSPSSLSASVGDRTITCRASQSINSYLDWYQQKPKAPKLLIYAASS  
 LQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYYSTPFTFGPGTKVEI  
 KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNS  
 QESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG  
 EC (SEQ ID NO:71)